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RESULT 2
US-09-949-016-11115
Sequence 11115, Application US/09949016
Parent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
ORGANISM: Homo sapiens
US-09-565-423-11
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Sequence 11115, A
Sequence 5, Appli
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                                                              February 26, 2005, 20:57:04; Search time 46.9787 Seconds (without alignments) 292.376 Million cell updates/sec
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Sequence 2, Ag
Sequence 2, Ag
Sequence 2671,
Sequence 2965,
Sequence 8740,
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964
1 MLQMAGQCSQNEYFDSLLHA......CKSLFAALSATEIEKSISAR 184
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Sequence 12,
Sequence 9,
Sequence 6,
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Sequence 11
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//cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

//cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

//cgn2_6/ptodata/1/iaa/8B_COMB.pep:*

//cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-11115
US-09-854-864-5
US-09-854-864-11
US-09-854-864-12
US-09-854-864-12
US-09-854-864-12
US-09-854-864-12
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US-09-854-864-10
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US-09-854-864-14
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US-09-489-039A-8740
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-09-107-433-2965
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Maximum Match 100%
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                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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No.
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Sequence 11, Application US/09565423

Sequence 11, Application US/09565423

Sequence 11, Application US/09565423

Sequence 11, Application US/09565423

SEQUENCE INFORMATION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND TITLE OF INVENTION: METHODS OF USE THEREOF

TITLE OF INVENTION: METHODS OF USE THEREOF

FILE REFERENCE: 2879-75.

CURRENT FILING DATE: 2000-05-05

PRIOR FILING DATE: 2000-05-06

PRIOR FILING DATE: 1999-05-06

NUMBER OF SEQ 1D NOS: 17

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 11

LENGTH: 184

TYPE: PRI
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Sequence 30, Appl
Sequence 5429, Ap
Sequence 2, Appli
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US-09-328-352-6022
US-09-321-160-18
US-09-854-864-11298
US-09-902-540-11298
US-09-780-717-44
US-09-854-864-20
US-09-810-572A-6
US-09-810-572A-6
US-09-854-864-15
US-09-65-911-30
US-09-65-911-30
US-09-65-481-6
US-08-660-148-5
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Sequence 11, Application US/09854864
Sequence 11, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS HOW GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILLE OF INVENTION: BLYS/AGP-3, AND TACI
FILLE REPERENCE: A-6868
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILLING DATE: 2000-05-12
PRIOR FILLING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR PILLING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Shu, Hong-Bing
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT APPLICATION NUMBER: UNKNOWN
PRIOR APPLICATION NUMBER: 00/132,892
PRIOR APPLICATION NUMBER: 60/132,892
PRIOR PLING DATE: 1999-05-06
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEC ID NOS: 17
SOFTWARE: PATENTIN VET: 2.1
   61 LIISLAVPVLMFLIRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILFRGLEYTV 120
                                                                                                                                          121 EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 180
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59 LVLSLALFTISFLLRKOMPEALKDEPQSPGQLDGSAQLDKADTELTRIRAGDDRIFPRSL 118
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Best Local Similarity 62.64
Matches 117; Conservative
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; ORGANISM: Mus musculus
US-09-565-423-17
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US-09-854-864-11
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS
APPLICANT: TY, GANG
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-666B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT PILING DATE: 2001-09-11
PRIOR PILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-27
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-31
SOFTWARE: PATENTIN VERSION 3.1
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PLING DATE: 2000-09-08
PRIOR PLING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR PLING DATE: 2000-10-03
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Pred. No. 1.1e-103;
Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.1
Matches 184; Conservative 0; Mismatches
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Sequence 5, Application US/09854864;
Patent No. 6774106;
GENERAL INFORMATION:
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US-09-854-864-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Human
US-09-949-016-11115
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Patent No. 6774106

Batent No. 6774106

GENERAL INCRMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

APPLICANT: THE OF INVENTION:

APPLICANT: THE OF INVENTION:

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-05-12

PRIOR PLING DATE: 2000-05-22

PRIOR PLING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 AVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 LIISLAVFVLMFLLRKISSEPLKDEPKNTGSG-------LLGMANIDLEKSRTG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 DTLMISRTPEVT---CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV 141
                                                                                                                                                                                                                                                                                                                                                           9 SONEYFDSILHACIPCOLRCSSNTPPLICORYCNASVTNSVKGTNAILWTCLGLSLIISL 68
                                                                                                                                                                                                                                                                                                                                                                                                    2 AQCEYPDSLLHAC-PC-LRCS----PPTCQ-YC--SVT-SVKGT---LW--LGL---LSL 43
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                                                                                                                                                                                                                                                                   Score 311.5; DB 4; Length 117;
Pred. No. 2.9e-28;
4; Mismatches 7; Indels 49
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  PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                            TYPE: PRT
ORGANISM: human-murine Consensus
                                                                                                                                                                                                                                                                   Query Match 32.3%;
Best Local Similarity 61.5%;
Matches 96; Conservative
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                                                                                                                                   SEQ ID NO 12
LENGTH: 117
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US-09-854-864-9
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LENGTH: 283
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APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REPERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEO ID NOS: 31
SOFTWARE: PATENTIN OFFICIAL OFFICE APPLICATION NUMBER: 13 31
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Barent No. 6774106

GENERAL INFORMATION:

APPLICANT: THELL, LARS EXDE

APPLICANT: YU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A6.868

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11
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                                                                                                                                                     ; Score 572; DB 4; Length 185;
; Pred. No. 3.3e-58;
21; Mismatches 41; Indels
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Best Local Similarity 100.0%; Pred. No. 5e-30;
Matches 58; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application US/09854864
Patent No. 6774106
                                                                                                                                                       59.3%;
SOFTWARE: PatentIn version 3.1 SEQ ID NO 11 '
                                                                                                                                                                                                   Conservative
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                                                                                                                                                   Query Match
Best Local Similarity
Matches 117; Conserv
                                                                                     ; ORGANISM: Murine US-09-854-864-11
                                              185
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LENGTH: 58
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TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MAITER CONCERNING AFRIL/G70, BCMA, TITLE OF INVENTION: BLYS/AGP-3, AND TACI
PILE REPERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATCHIN USER: US 60/214,591
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATCHIN USER: US 60/214,591
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REPERENCE: A-6868
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-05-13
RIOR PILING DATE: 2000-05-13
SUPPRIOR FILING DATE: 2000-05-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 201; DB 4; Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.2e-15;
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Patent No. 6774106
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Best Local Similarity 100.
Matches 34; Conservative
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Best Local Similarity
Matches 64; Conserv
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ORGANISM: Consensus
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Sequence 7, Application US/09854864

Sequence No. 6774106

GENERAL INFORMATION.

APPLICANT: THEILL, LARS EXDE

APPLICANT: THEILL, LARS EXDE

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: MUBBER: US/99/854,864

CURRENT APPLICATION NUMBER: US 60/204,039

PRIOR PILING DATE: 2000-05-12

PRIOR PPLICATION NUMBER: US 60/204,039

PRIOR PILING DATE: 2000-06-27

PRIOR PPLICATION NUMBER: US 60/214,591

PRIOR PLING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PATENTH NOS: 31

SSCTIMARE: PATENTH NOS: 31

SSCTIMARE: PATENTH NOS: 31
                                                                                                     GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLSS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT PAPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR PELING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ!ID NOS: 31
SSOTWARE: Patentin version 3.1
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29.5%; Score 284; DB 4; L
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 51; Conservative 0; Mismatches 0;
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                                                        Sequence 6, Application US/09854864
Patent No. 6774106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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Best Local Similarity
Matches 34; Conserva
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US-09-854-864-13
                         JS-09-854-864-6
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---TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
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                                                                                                                                                                             Query Match 8.2%; Score 79.5; DB 2; Length 1009; Best Local Similarity 32.1%; Pred. No. 5.4; Matches 25; Conservative 9; Mismatches 29; Indels 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
8.2%; Score 79.5; DB 2; Length 1009;
Best Local Similarity 32.1%; Pred. No. 5.4;
Matches 25; Conservative 9; Mismatches 29; Indels 15
                                                                                                                                                                                                                            29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08460626

Patent No. 5837815

GENERAL INFORMATION:
APPLICANT: SIMA LEV
APPLICANT: JOSEPH SCHLESSINGER
TITLE OF INVENTION: PYK-2 RELATED PRODUCTS AND
STREET: Lyon & Lyon
STREET: 134 West Fifth Street
STREET: 634 West Fifth Street
STREET: 634 West Fifth Street
STREET: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: BACCARGE
COMPUTER: LBM COMPATION: 435
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,626
FILING DATE: June 2, 1995
CLASSIFICATION NUMBER: 08/357,642
FILING DATE: December 15, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J
REFERENCE/DACKEY NUMBER: 3.17773
                                                                                                                                                                                                                                                                            88 EFKNTGSGLLGMANIDLEKSR-----
                                                                                                                                                                                                                                                                                                                                                                            139 DSDHCFPLPAMEEGATIL 156
                                                                                                                                                                                                                                                                                                                                                                                                                         306 RŚIRCLPĽ---ÉEGOAVĽ 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            relecommunication information:
Telephone: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELES: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-357-642A-1
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US-09-854-864-8

| Sequence 8, Application US/09854864
| Sequence 8, Application US/09854864
| Sequence 8, Application US/09854864
| Setting No. 6774106
| GENERAL INFORMATION:
| APPLICANT: THEILL, LARS EYDE
| APPLICANT: YU, GANG
| TITLE OF INVANTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, ECMA,
| TITLE OF INVANTION: BLYS/AGP-3, AND TACI
| FILE REFERENCE: A-6868
| CURRENT APPLICATION NUMBER: US/09/854,864
| CURRENT FILING DATE: 2001-09-11
| PRIOR PILING DATE: 2000-05-12
| PRIOR PILING DATE: 2000-05-12
| PRIOR PILING DATE: 2000-06-27
| WINDER OF SEQ ID NOS: 31
| SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sima Lev
APPLICANT: Joseph Schlessinger
TITLE OF INVENTION: PYKZ RELATED PRODUCTS
TITLE OF INVENTION: AND METHODS
UNMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/357,642A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 ILWICLGLSLIISLAVFVLMF 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          December 15, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 209/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Sulte
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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US-08-357-642A-1
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139 DSDHCFPLPAMEEGATIL 156
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Search completed: February 26, 2005, 21:06:28 Job time : 47.9787 secs

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2005, 20:24:52; Search time 194.962 Seconds (without alignments) 365.015 Million cell updates/sec
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5.1.6
Compugen Ltd.
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 GenCore version
Copyright (c) 1993 - 2005
                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
                                                                                                           February 26,
                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                         Scoring table:
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geneseqp2003as:*geneseqp2003bs:* geneseqp1990s:* geneseqp2000s:* geneseqp20018:* geneseqp20028:* geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is defived by analysis of the total score distribution.

SUMMARIES

	Description	Aab08843 Amino aci	Aav94001 A human B		9 Human		Aae00506 Human B c	Abb81487 Human BCM	Abp54694 Metastati			-	_			Human	Adk00756 Native hu		Adp56014 Human PRO		Human			Aab08844 Amino aci	Aay71980 Murine B	Aae15490 Mouse B c
	ID	AAB08843	AAY94001	AAE09241	AAY71979	AAB60698	AAE00506	ABB81487	ABP54694	AAE28961	AAE35216	ADA49361	ABP60552	ABP97717	ADD67527	ADG43715	ADK00756	ADQ94442	ADP56014	ABR40082	ABG95060	AAE15484	AAB60700	AAB08844	AAY71980	AAE15490
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مد	Match	100.0	0.001	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.4	99.1	98.5	74.6	59.3	59.3	59.3
	Score	964	964	964	964	964	964	964	964	964	964	964	964	964	964	964	964	964	964	958	955	950	719.5	572	572	572
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Aae15491 Human B c Aae16491 Human-mur Aab60699 Mouse IgG Aae00507 Human BCM Ad431717 Human BCM Aae15488 Human BCM Aae15486 Human BCM Aae15486 Human BCM Aae15489 Mouse BCM Aae15499 Mouse BCM Abj38417 TALL-1 re Adj38417 TALL	Aae15487 Human B-c Aae22269 Human BAF
AAE15501 AAE15491 AAB00509 AAB00507 AAE1548 AAE1548 AAE1548 AAE1548 AAE1548 AAE1548 AAE2244 ABB1489 ABB1489 ABB1489 ABB1489 ABB22266	AAE15487 AAE22269
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286.5 286.5 286.5 286.5 286.5 201 101 101 101 101 101 101 101 101 101	104 103.5
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ALIGNMENTS

RESULT 1

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* geneseqp1980s:*

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Database

BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; septic shock. 57. .77 /note= "putative transmembrane domain" Location/Qualifiers AAB08843 standard; peptide; 184 AA. Amino acid sequence of human. 24-FEB-2000; 2000WO-US004925. 99US-0121485P. (first entry) (GEHO) GEN HOSPITAL CORP. Ting A; WO200050633-A1 Homo sapiens. 24-FEB-1999; 02-JAN-2001 31-AUG-2000. AAB08843; Seed B, Key Domain

WPI; 2000-558405/51.

Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene expression.

Claim 32; Fig 7A; 53pp; English.

The present sequence represents a BCMA (not defined) polypeptide. BCMA is a necrosis factor (NF)-kB activator. The method of the invention is used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a recombinant anti-cell death gene and a reporter gene operably linked to

renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

Disclosure; Page 152; 175pp; English

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Human, BR43x2; TACI receptor; extracellular domain; BCMA, B cell protein; transmembrane activator and CAML-interactor; tumour necrosis factor; TNF; strif4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; emphysema; pyelonephritis; renal neoplasm; multiple myelomephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCWA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid archritis, inflammatory bowel disease or septic shock. BCWA is useful for inflammatory compounds that modulate NF-kB expression and thus for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
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; Score 964; DB 3;
; Pred. No. 1e-94;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 184; Conservative 0
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The present sequence represents a human BCMA protein, a B cell protein related to transmembrane activator and CAML-interactor (TACI) receptor. Tract is a tumour necrosis factor (TNF) receptor. The extracellular committee of insoform of TACI). TACI on BCMA (a related B cell protein) receptor contain a cysteine rich domain, and are used for inhibiting zinf4 activity. Zinf4 is a TNF ligand. They may also be used for inhibiting zinf4 activity. Zinf4 is a TNF ligand. They may also be used for inhibiting zinf4 activity. Zinf4 is a TNF ligand. They may also be used for inhibiting BR43X2, TACI or BCMA receptor-ligand engagement associated with antibody production. The antibody production is associated with antibody production. The antibody production is associated with antibody production. The mithody production is associated with antibody production and rheumatoid arthritis. The zinf4 activity and BR43x2. TACI or BCMA receptor-ligand engagement is associated with asthma, bronchitis, emphysema, end stage renal failure, and stage renal failure, colomeraling immune response, immunosuppression, graft crejection, graft versus host disease, inflammation, insulin dependent colomes shock. BR43x2, TACI, and BCMA polypeptides, funsions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery cremases, or occlusion, and cholesterol or renal emboli
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100.0%; Pred. No. 1e-94;
ive 0; Mismatches 0
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Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,

N-PSDB; AAA58559

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07-JAN-2000; 2000WO-US000396

13-JUL-2000

99US-00226533

07-JAN-1999;

(ZYMO) ZYMOGENETICS INC. Gross JA, Xu W, Madden WPI; 2000-452538/39. Location/Qualifiers

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Key
Domain
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                                                                                                                                                                                                                                                   The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseased associated with increased TALL-1 and APRIL expression or between APRIL and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The present sequence is human BCMA protein
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                                                            Pitti RM;
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                                                                                                                                               Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
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                                                            Kim KJ, Marsters SA,
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                                                            Grewal I,
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22-AUG-2000; 2000US-0226986P
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                                                           Dodge KH,
                            (GETH ) GENENTECH INC
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                                                         Ashkenazi AJ,
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The present invention relates to Tumour necrosis factor (TNF) and Apol-
related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
crelated Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
creptiates (including homologues), and their antibodies. The invention in
particular relates to methods for regulating the interaction between TALL-
cregulate monocyte, macrophage and B lymphocyte mediated immune responses.
CT TALL-1 protein is useful for identifying compounds that regulate B
TYALL-1 protein is useful for identifying compounds that regulate B
CC speciated autoimmune disorders like rheumatoid arthritis, systemic lupus
crythematosus (SLB), insulin dependent diabetes multiple
crythematosus (SLB), insulin dependent diabetes multiple
sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
canemia, autoimmune thrombocytcopenia purpura, Goodpasture's syndrome,
compensional mucleic acid sequence are also useful in diagnostic assays.
COPTENDIATION multiple acid sequence are also useful in diagnostic assays.
CT he present sequence is a human B cell maturation factor (BCMA) protein.
CT is the receptor for TALL-1 protein. BCMA gene is located on chromosome
CC in in human tissues, BCMA is expressed by spleen and lymph nodes but not
CMA mRNA is absent in the pro-B lymphocyte stege but its expression
cc increases with B lymphocyte maturation
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Best Local Similarity , 100.0%; Pred. No. 1e-94;
Matches 184; Conservative 0; Mismatcher
1. .62
/label= Extracellular_domain
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AAB60698 standard; protein; 184 AA Homo sapiens. 22-MAY-2001 Thompson J; 22-FEB-2001 Mackay F, AAB60698;

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                                                                                                                                                                                                                                                                                                                                                                                                   Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immuno-related disorder; B-cell growth inhibitor; BCWA; b-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell Jymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents human BAFF-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 964; DB 4; Length 184; 100.0%; Pred. No. 1e-94; tive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lymphoma; gene therapy; cancer; tumour.
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11-FEB-2000; 2000US-0181684P.
18-FEB-2000; 2000US-0183536P.
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                                                                                                                                                                                                                                                                                                            Human BAFF receptor (BAFF-R)
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Query Match 100. Best Local Similarity 100. Matches 184; Conservative

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The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (BCM or BCMA) antegonist that antegonises the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinoma, colon carcinoma, press carcinoma, and other carcinoma e.g. modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferation such as cancer or carcinoma, comprises administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
                                                   GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
                                                                                                                               121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
                                                                                                                                                      120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic; gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease; B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF; tumour necrosis factor; BCMA; B cell maturation protein.
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1 MLQWAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
                                                                            61 GLSLIISLAVFVIMFLIRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
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proliferation such as cancer or carcinoma, comprises administeri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human B cell maturation protein (BCMA).
                                                                                                                                                                                                                                                                                                                                                            AAE00506 standard; protein; 184 AA.
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11-FEB-2000; 2000US-0181807P.
30-JUN-2000; 2000US-0215688P.
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(APOT-) APOTECH R & D SA.
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disease, systemic lupus erythematosus-SLE); hypertension, cardiovascular diseases, renal disorders, B-cell lympho-proliferative disorders, limmunosuppressive diseases, organ transplantation, inflammation and human immunodeficiency virus (HIV), and for treating, suppressing or altering an immune response involving a signalling pathway between APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy. The present sequence is human APRIL-R also referred as BCMA or BCM protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Ztnfr12; tumour necrosis factor receptor; cytostatic; immunosuppressive; dermatological; antinflammatory; antidabetic; neuroprotective; antisheumatic; antiarthritic; antiasthmatic; nephrotropic; hypotenaive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthemia gravis; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis; pyelonephritis; renal neoplasm; multiphe myeloma; amyloidosis; light chain neuropathy; hypertension; large vessel disease; graft-versus host disease; graft rejection; Crohn's disease.
                                                                                                                                                                                                                                                                            1 MIQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
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20-DEC-2000; 2000US-0257131P.
28-UIM-2001; 2001US-0301715P.
29-AUG-2001; 2001US-0315565P.
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Matches 184; Conservative
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                                                                                                                                                           Sequence 184 AA;
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The present invention describes a numan tumour necrois receptor designated Zinfill (1). (1) has cytostatic, immunosuppressive, dermatological, antinflammatory, neuroprotective, antidiabetic, antiatrhatic, antiatrhamic, antiatrhamic, antiatrhamic, antiatrhamic, and and hypotensive activities, and can be used in gene therapy. (1) can be used for inhibiting, in a mammal, the activity of a ligand that binds Zinfill (e.g. Tinfill,) for treating disorders and diseases associated with B lymphocytes, activated B lymphocytes, activated B lymphocytes, activated B lymphocytes, resting B lymphocytes, and for inhibiting the proliferation of tumour cells. (1) is useful for treating cutoimmune disorders such as systemic lupus erythematosus, myasthemia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, theumatoid arthritis, bronchitis, emphysema and end stage renal failure cor renal disease such as systemic lupus erythematosus, myasthemia gravis, multiple myelomas, lymphomas, light chain neuropathy, or neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel diseases, graft-versus host disease, graft rejection and Crohn's disease, (1) is useful for modulating the immune system, for regulating B cell responses and development, for modulating development of other cells, antibody production and cytokine production, and for modulating T and B cell communication. The present sequence represents a protein which is given in the exemplification of the present invention
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Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage
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                 renal failure or renal disease and lymphoma
                                                            English
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                                                            Disclosure; Page 135-136; 154pp;
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Best Local Similarity
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The invention relates to the manufacture of a composition for inhibiting the proliferation of tumour cells. The method involves using an antibody component that binds both the B-cell maturation antigen (BCMA) and the transmembrane activator and calcium-modulator and cyclophilin ligand-interactor (TACI). BCMA and TACI binding antibody compositions are useful for inhibiting proliferation of tumour cells, particularly inhibiting ZTNF4 activity in a mammal associated with increased endogenous antibody production or a disorder consisting of neoplasm, chronic lymphocytic leukaemia, multiple myeloma, non-fledgkin's lymphome, post-transplantation lymphoproliferative disease or light chain gammopathy or inflammation e.g. asthma. The invention is also useful in gene therapy. The present is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLSLIISLAVFVIMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEILLPRGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                 B-cell maturation antigen and transmembrane activator and calcium-
modulator and cyclophilin ligand-interactor, useful for treating
disorders e.g. inflammation or lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 964; DB 5;
100.0%; Pred. No. 1e-94;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human B-cell maturation receptor (BCMA) protein.
                        "Cysteine rich, region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 63; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE35216 standard; protein; 184 AA.
                                                                                                                                                                                               20-FEB-2001; 2001US-0270274P. 12-APR-2001; 2001US-0283447P.
                                                                                                                                                      06-FEB-2002; 2002WO-US003500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 184; Conservative
                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-723183/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human BCMA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD46410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 184 AA;
                                                                 WO200266516-A2
                                                                                                                                                                                                                                                                                                         Kindsvogel W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAY-2003
                                                                                                         29-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the protein sequence of a human polypeptide encoded by a gene that exhibits decreased expression in colon cancerderived metastages compared to normal colon tissue. It is an example of claimed polypeptides that are encoded by genes which are differentially expressed in metastatic colorectal cancer cells. Such polypeptides are useful in diagnostic and prognetic assays, for raising antibodies useful e.g. in immunotherapy, and in screening for modulator compounds of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
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                                                                                                                                                                                                                                     New genes that are up- or down-regulated in colorectal cancer, useful for diagnosing colorectal cancer in a subject, or for identifying modulators of colorectal cancer-associated proteins and genes for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLICQRYCNASVTNSVKGTNAILMTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; tumour; B-cell maturation antigen; transmembrane activator; calcium-modulator; cyclophilin ligand-interactor; TAC1; gene therapy; neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease; non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 964; DB 5; Length 184; 100.0%; Pred. No. 1e-94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Antigenic epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human B-cell maturation antigen (BCMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAE28961 standard; protein; 184 AA.
                                                               EOS BIOTECHNOLOGY INC.
UNIV CASE WESTERN RESERVE.
                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 255; 260pp; English.
02-APR-2001; 2001US-0281149P
17-APR-2001; 2001US-0284555P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 184; Conservative
                                                                                                                                Markowitz SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCMA; multiple myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 54
                                                                                                                                                                        WPI; 2002-698677/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                         colorectal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapeutic value
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                                                                                                                                                                                               N-PSDB; ABQ81560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                Mack DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                 EOSB-)
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Gaps

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20-NOV-2003 (first entry)

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The invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumnour necrosis factor-like protein (ZTNF)2 or ZTNF4; and an immunoglobulin group comprising a constant region of an immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumour cells in a mammalian subject. The composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic lupus erythematosus, multiple aclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft rejection, anaemia and septic shock. The fusion proteins are also used in gene therapy. The present sequence is human B-cell maturation receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane activator and calcium modulator and cyclophilin ligand-
interactor (TACI)-immunoglobulin fusion protein, for treating cancer or
diabetes, domprises a TACI receptor group and an immunoglobulin group.
anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive; glomerulonephritis; asthma; bronchitis; graft rejection; septic shock; dermatological; neuroprotective; cyclophilin ligand-interactor; human; autoinmune disease; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
                                                                                                                  B-cell maturation receptor; BCMA; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yene therapy. The present sequence i (BCMA) protein used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Col 100; 71pp; English.
                                                                                                                                                                                                                                                                                            20-MAY-2003; 2002WO-US015910.
                                                                                                                                                                                                                                                                                                                                         24-MAY-2001; 2001US-0293343P.
                                                                                                                                                                                                                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Rixon MW, Gross JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-148455/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD53754
                                                                                                                                                                                                    WO200294852-A2
                                                                                                                                                              Homo sapieris
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ö 120 120 180 180 09 9 1 MLQMAGQCSQNEYFDSLLHACIPCQRCSSNTPPLTCQRYCNASVTNSVKGTNALLWTCL GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE GLSLISLAVFVLMFLLRKISSEPLXDEFXNTGSGLLGMANIDLEKSRTGDEILLPRGLE 121 YTVEECTCEDCIKSKPKVDSDHCPPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL Gaps ö 100.0%; Score 964; DB 6; Length 184; 100.0%; Pred. No. 1e-94; tive 0; Mismatches 0; Indels (Query Match
Best Local Similarity 100.
Matches 184; Conservative ISAR 184 184 Sequence 184 AA; ISAR 121 61 61 181 181 8 셤 ò ద 8 셤 8 요

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The invention relates to a novel TALL-1 antagonist protein, comprising a sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID NO:2, by at least one modification in the region connecting &bgr; strands D and E that reduces the biological activity of the TALL-1 antagonist as compared to wild-type TALL-1. A protein of the invention has immunosuppressive, antirheumatic, antinflammatory, antiarthritic, dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic, nephrotropic, and vasotropic activity, A TALL-1 antagonist may be used in a vaccine. A protein of the invention is useful for inhibiting TALL-1 biological activity in a mammal. TC is useful for inhibiting TALL-1 chematoid arthritis, systemic lupus erythematosus, insulin dependent diabetes mellitus, multiple sclerosis myasthaenia gravis, cave, s disease, autoimmune hemolytic anaemia, autoimmune thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris, auter rheumatic fever, post-streptococcal glomerulonephritis and course rheumatic fever, post-streptococcal glomerulonephritis and polyarteritis nodosa. The present sequence represents human BCWA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological activity in mammal, has a modification in the region connecting beta strands D and E that reduces the biological activity of TALL-1
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                                                                                      human; TALL-1; antagonist; immunosuppressive; antirheumatic; antiinflammatory; antiinflammatory; antiinflammatory; antiinflammatory; antiinflammatory; antithyroid; antipyretic; nephrotropic; vasotropic; vaccine; autoimmune disease; rheumatoid arthriti; systemic lupus erythematosus; insulin dependent diabetes mellitus; multiple sclerosis; mysthaenia gravis; Grave's disease; autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura; Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCWA.
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14-JAN-2002; 2002US-0348962P.
07-FEB-2002; 2002US-0354966P.
13-AUG-2002; 2002US-0403364P.
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ADA49361 standard; protein; 184 AA.

RESULT 11 ADA49361 ADA49361;

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The invention relates to a novel antibody or its fragment, which immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL). The antibody of the invention has dermachological, immunosuppressive, antiallammatory, antiarthritic, cytostatic, antianaemic, antiallammatory, antiathmatic, neuroprotective, ophthalmological, uniallaric, antiallaric, antiallaric, antianteriosclerotic, usectropic, thyromimetic, and haemostatic activity. Cut antiarteriosclerotic, vasotropic, thyromimetic, and haemostatic activity. The antibody or its fragment are useful for treating, preventing or ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in host disease (GVHD). The autoimmune disease, and graft versus cort thematosus, rheumatoid arthritis or Sjogren's syndrome. The antibody captured antiorating adisease or disorder associated with aberrant APRIL or APRIL receptor expression or aberrant function of APRIL or APRIL ceceptor expression or aberrant function of APRIL or APRIL ceceptor expression or aberrant function of APRIL or APRIL ceceptor. The disease or disorders includes autoimmune and inflammatory disorders such as autoimmune neutropenia, haemolytic anaemia, dermatitis, ashmin allergic encephalomyelitis, myocarditis, multiple sclerosis, uveitis, tuberculosis, diabetes mellitus, psoriasis, cancer of the immune gravis, Hashimoto's disease, immunodeficiency syndrome (AIDS)), and proliferative disorders (e.g. leukemia). The present sequence represents
GVHD;
                                                                                                                                                                                                                                                                                                                                                                                                                      dermatological; immunosuppressive; antiinflammatory; antirheumatic; antiantrité, gytostatit; antianaemic; antiantergic; antiantentité, cytostatit; antiantement; antiantergic; antidiabetic; antipsoriatic; ophinalmological; tuberculostatic; antidiabetic; antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic; hameostatic; cancer; autoimmune disease; graft versus host disease; GVHD inflammatory disorder; proliferative disorder; single chain antibody; antibody; human; BCMA; tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor delta, useful for treating, preventing or ameliorating Non-
Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
                                                                                                                                                                                                                                                                                                                                                                                               scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated antibody that immunospecifically binds tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Page 222; 225pp; English.
                                                                                                                                                                                                                   ABP60552 standard; protein; 184 AA.
                                                                                                                                                                                                                                                                                                                                                      necrosis factor BCMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAY-2002; 2002WO-US016106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-2001; 2001US-0293100P
                                                                                                                                                                                                                                                                                                           28-MAR-2003: (first entry)
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                                                                 181 ISAR 184
                                                                                                          İSAR 184
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                                                                                                                                                                                                                                                                                                                                                      Human tumour
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                                                                                                                                                                                                                                                                ABP60552;
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                                                                                                                                                                                              61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
                                                                                                                                                                                                                                         The present sequence represents a human BCMA polypeptide. The specification also describes TACI and BR3 polypeptides. TACI and BR3 are receptors. Tumour necrosis factor (TNP) family ligands TALL-1 and April bind to the TACI receptor, while TNF family ligands TALL-1 also binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for
                                                                                                              09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, TACI, BR3, receptor; tumour necrosis factor ligand, TNF ligand,
TALL-1; April; systemic lupus erythematosus; BCMA.
                                                                                                                                                                                                                           121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
                                                                                                                                       1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
                                                                                                             1 MIQMAGQCSQNEYFDSILHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding a TACIs or BR3 polypeptide, useful for preparing a composition for treating systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preparing a composition for treating systemic lupus erythematosus
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                                                     Length 184;
                                                                                 Indels
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                                                     DB 6;
                                                      Score 964; DB 6
Pred. No. 1e-94;
                                          100.0%; bcc.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of human BCMA receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yan M;
                                                                                                                                                                                                                                                                                                                                                                                     ABP97717 standard; protein; 184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 2; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ridgway J,
the tumour necrosis factor BCMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2001; 2001US-0310114P. 30-APR-2002; 2002US-0377171P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-2002; 2002WO-US023487.
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Best Local Similarity 100.
Matches 184; Conservative
                                                                  Best Local Similarity 100.
Matches 184; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dixit V, Grewal I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-256560/25.
                                                                                                                                                                                                                                                                                     184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 184 AA;
                            Sequence 184 AA;
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                                                        Query Match
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screening anti-jugates for treating

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The polynucleotide (I) or polypeptide can be used for screening anti-
cancer agents, and generating antibodies or immunoconjugates for treating
or preventing the above-mentioned diseases. The polynucleotide,
polypeptide or antibody can be used for detecting, diagnosing or
prognosticating the haematological malignancies described above. The
present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADG43715 standard; protein; 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2003; 2003WO-US005147
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                                                                                                                                                                                                                                                                                                                                                                      ISAR 184
                                                                                                                                                                                                                                                                                                                                                                                                 181 ISAR 184
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                                                                                                       Sequence 184 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an isolated polynucleotide (I), which is overexpressed in haematological malignancies, and which encodes a polypeptide or an immunogenic fragment of the polypeptide. Also comprising (I) operably linked to an expression vector comprising (I) operably linked to an expression control sequence; (3) a host cell.comprising an expression vector; (4) an isolated antibody that comprising to the polypeptide or its immunogenic fragment; and (5) immunoconjugates comprising the antibody above, or an antibody that specifically binds to a polypeptide, or its immunogenic fragment, encoded (5) immunoconjugates and immunostimulant activities, and can be used in vaccines and immunotherapy. The immunoconjugates are useful in the manufacture of a medicament, particularly as active ingredients in a composition for treating canent, e.g. multiple myeloma cell, chronic lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep, lymphocytic leukaemia, equines, porcines, lupines, canines or felines.
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                                                                                                                                                                                                                                                                                                                                                                                                                  haematological malignancy; immunoconjugate; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine; immunotherapy; cancer; multiple myeloma cell;
chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
                                                                          GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
                                                                                           GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
                                                                                                                                    YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
                                                                                                                                                    YTVECTCEDCIKSKPKVDSDHCPPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKS
                  MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New hematological malignancy-related genes and polypeptides, useful screening anti-cancer agents, and generating antibodies or immunoconjugates for treating e.g. multiple myeloma cell or chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ordonez N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clapper JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; SEQ ID NO 4; 307pp; English.
                                                                                                                                                                                                                                                                                              ADD67527 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                   Human Ly1732P protein SEQ ID NO:4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-JAN-2003; 2003WO-US002353
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Mcneill PD;
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Carter L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; neurodegenerative immunological disorder; demyelination;
Central Nervous System; CNS; inflammation; B-cell maturation antigen;
BCMA; multiple sclerosis; neuroprotective; nootropic; antiinflammatory;
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Length 184;
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0; Mismatches 0;
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Query Match 100.0%; Score 964; Best Local Similarity 100.0%; Pred. No. 16 Matches 184; Conservative 0; Mismatches
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method of the invention has neuroprotective, nootropic, and antinflammatory activity, and may have a use in gene therapy. The methods, BCMA, and antibodies are useful for treating a neurodegenerative immunological disorder such as multiple sclerosis, demyelination or CNS inflammation. The present sequence represents human BCMA.
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Sequence 184 AA;

ö Gaps ö Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 1e-94;

Matches 184; Conservative 0; Mismatches 0; Indels (

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1 MLQWAGQCSQNEYFDSLLHA......CKSLFAALSATEIEKSISAR 184
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/cgn2_o/ptodata/1/pubpaa/USIOU_PUBCOMB.pep:
/cgn2_o/ptodata/1/pubpaa/USIONEW_PUB.pep:
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/cgn2_o/ptodata/1/pubpaa/USiONEW_PUB.pep:*
/cgn2_o/ptodata/1/pubpaa/USiONEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 1, Appli	Sequence 7, Appli	Sequence 1, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 47, Appl	Sequence 8; Appli	Sequence 7, Appli	Sequence 27, Appl	Sequence 11, Appl	Sequence 39, Appl	Sequence 5, Appli	Sequence 5, Appli
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ΩΙ	US-10-077-438-1	US-10-077-438-7	US-10-077-137-1	US-10-077-137-7	US-10-068-725-2	US-10-151-882-47	US-10-115-192-8	US-10-008-063-7	US-10-152-363A-27	US-10-216-074-11	US-10-087-080-39	US-09-854-864-5	US-09-855-158-5
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% Query Match Length DB	184	184	184	184	184	184	184	184	184	184	184	181	181
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.5	98.5
Score	964	964	964	964	964	964	964	964	964	964	964	950	950
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Length 184; Indels

Sequence 11, Appl	11,	_	2	Sequence 21, Appl	H	ñ	9	ຄັ	ō	ω̈	ø	(n)	٠.,	-	<u>-</u>	H	H	ĭ	ĭ	о О	_	٠ı	н	æ	8	Sequence 2, Appli	'n	ŏ	ς,	09	Sequence 10, Appl
US-09-854-864-11	19-855-	4 US-10-216-074-17	_			US-09-855-158-	4	US-09-854-		US-09-854-864-6	US-09-855	13 US-10-077-438-3	US-10-077-13	US-09-854-864		US-09-854-864-13			₽	.4 US-10-145-206-197		.5 US-10-380-703-9		US-09-854-864-8	US-09-855-158-8		ns-	.3 US-10-087-192-984	ns-	10-152-363A-	.5 US-10-380-703-10
185 9	185 9	185 1				117 9	•		283,9			•	207 1			81 9		281 9		42 1	•	175 1	175 1	21 9	21 9	185 1	185 1	184 1	184 1	184 1	184 1
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ALIGNMENTS

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Query Match
100.0%; Score 964; DB 13;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 184; Conservative 0; Mismatches 0;
                                                                                                                                                            APPLICANT: MacKay, Fallenie
APPLICANT: MacKay, Fallenie
APPLICANT: Tachopp, Jurg
APPLICANT: Tachopp, Jurg
APPLICANT: Tachopp, Jurg
APPLICANT: Thompson, Jeffrey
APPLICANT: Schneider, Pascal
APPLICANT: Boggen, Inc.
APPLICANT: Baggen, Inc.
APPLICANT: Baggen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immunoregulatory Agent
FILE REFERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077,438
CURRENT APPLICATION NUMBER: 60/149,378
PRIOR PILING DATE: 1999-08-17
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-118
PRIOR FILING DATE: 2000-02-118
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                 Sequence 1, Application US/10077438; Publication No. US20020165156A1; GENERAL INFORMATION:
                                                                                                                                             APPLICANT: MacKay, Fabienne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: homo sapien
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RESULT 1
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                                                                                                                                                                                                                               APPLICANT: Incubson, Usility
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immunoregulatory Agent
FILE OF INVENTION: Immunoregulatory Agent
FILE REFERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077,137
CURRENT FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Ambrose, Christine
APPLICANT: Ambrose, Christine
APPLICANT: Schneider, Pascal
APPLICANT: Tschopp, Jurg
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
ITILE OF INVENTION: Baff Receptor (BCWA), An
ITILE OF INVENTION: Immunoregulatory Agent
FILE REFERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077,137
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PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536
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                                                              APPLICANT: MacKay, Rabienne
APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Tschopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
Publication No. US20020172674A1
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CORGANISM: homo sapien
US-10-077-137-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/10077438
Publication No. US2020165156A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: MacKay, Fabienne
APPLICANT: Ambrose, Christine
APPLICANT: Tschopp, Jurg
APPLICANT: Tschopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Biogen, Inc.
APPLICANT: Appecen, Inc.
APPLICANT: Appecen, Inc.
APPLICANT: Appecen, Inc.
APPLICANT: Appecen, Inc.
APPLICANT: Applicant Applicant Applicant Applicant
APPLICANT: Applicant Applicant
APPLICANT: Applicant Applicant
APPLICANT: Applicant Applicant
CURRENT APPLICATION NUMBER: 60/149,378
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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US-10-077-137-1
; Sequence 1, Application US/10077137
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ORGANISM: homo sapien
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Best Local Similarity 100.
Matches 184; Conservative
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Best Local Similarity 100.
Matches 184; Conservative
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                                                                                                                                                             Length 184;
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## TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
## FILE REFERENCE: 01-04
## CURRENT APPLICATION
## CURRENT FILING DATE: 2002-02-06
## PRIOR APPLICATION NUMBER: 60/270,274
## PRIOR FILING DATE: 2001-02-20
## PRIOR FILING DATE: 2001-04-12
## PRIOR FILING DATE: 2001-04-12
## NUMBER OF SEQ ID NOS: 5
## SEQ ID NO 2
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100.0%; Pred. No. 1.9e-90;
Ative 0; Mismatches 0;
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100.0%; Score 964; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.9e-90;
Matches 184; Conservative 0; Mismatches 0;
PRIOR FILING'DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10068725 Publication No. US20030012783A1 GENERAL INFORMATION:
                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 184; Conservative
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                                                                                   TYPE: PRT
CORGANISM: hdmo sapien
US-10-077-137-7
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Sequence 47, Application US/10151882
| Sequence 47, Application US/10151882
| Publication No. US20030059862A1
| RENERAL INFORMATION:
| APPLICANT: Ruben, Steven M.
| TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
| FILE REFERENCE: PF554
| CURRENT APPLICATION NUMBER: US/10/151,882
| CURRENT FILING DATE: 2001-05-24
| PRIOR APPLICATION NUMBER: 60/293,100
| PRIOR APPLICATION NUMBER: 60/293,100
| PRIOR FILING DATE: 2001-05-24
| NUMBER OF SEQ ID NOS: 48
| SEQ ID NO 47
| LENGTH: 184
| TYPE: PRT
| ORGANISM: Homo sapiens
| US-10-151-882-47
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Sequence 8, Application US/10115192

Publication No. US20030082175A1

GENERAL INFORMATION:

APPLICANT: Applech R & D S.A.

TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof

TITLE OF INVENTION: April Receptor (CURRENT PILIUR DATE: 2002-04-02

PRIOR APPLICATION NUMBER: 60/215688

PRIOR APPLICATION NUMBER: 60/215688

PRIOR APPLICATION NUMBER: 60/181807

PRIOR APPLICATION NUMBER: 60/181807

PRIOR APPLICATION NUMBER: 60/181807

PRIOR APPLICATION NUMBER: 60/181807

PRIOR APPLICATION NUMBER: 60/181807

PRIOR APPLICATION NUMBER: 60/181807

PRIOR APPLICATION NUMBER: 60/181907

PRIOR APPLICATION NUMBER: 60/181907

PRIOR APPLICATION NUMBER: 60/181907

PRIOR APPLICATION NUMBER: 60/18193

PRIOR FILING DATE: 1999-10-06

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

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100.0%; Pred. No. 1.9e-90;
ive 0; Mismatches 0;
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100.0%; Pred. No. 1.9e-90;
tive 0; Mismatches 0;
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RESULT 11
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GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
                61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
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                                                                                                                                                                                                                          Sequence 7. Application US/10008063
; Publication No. US20030092164A1
; GENERAL INFORMATION:
APPLICANT: Gross, Jane A.
; APPLICANT: Wenfeng
APPLICANT: Grant, Francis, J.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor;
FILE REFERENCE: 00-103
CURRENT FALING DATE: 2001-11-05
; UNMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-152-363A-27
Sequence 27, Application US/10152363A
Publication No. US20030103986A1
GENERAL INFORMATION:
APPLICANT: Rixon, Mark W.
ITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
FILE REPERENCE: 01-20
CURRENT APPLICATION NUMBER: US/10/152,363A
CURRENT FILING DATE: 2002-05-20
PRIOR PILICATION NUMBER: 60/293,343
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 70
SSEQ ID NOS: 70
SSEQ ID NO 27
LENGTH: 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-008-063-7
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TYPE: PRT
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US-10-008-063-7
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Sequence 11, Application US/10216074;
Publication No. US20030148445A1;
Publication No. US20030148445A1;
Fublication No. US20030148445A1;
FUBLICANT: Shu, Hong-Bing;
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND TITLE OF INVENTION: METHODS OF USE THEREOF;
TITLE OF INVENTION: METHODS OF USE THEREOF;
CURRENT APPLICATION NUMBER: US/10/216,074;
CURRENT FILING DATE: 2003-03-12;
PRIOR APPLICATION NUMBER: US/09/565,423;
PRIOR APPLICATION NUMBER: UNKNOWN;
PRIOR FILING DATE: 2000-05-01;
PRIOR FILING DATE: 2000-05-01;
PRIOR FILING DATE: 1999-05-06;
NUMBER OF SEQ ID NOS: 17;
SOFTWARE: Patentin Ver. 2.1;
SEQ ID NO 11;
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                                                                              Length 184;
                                                                                                                           Indels
                                                                              Query Match 100.0%; Score 964; DB 14; Best Local Similarity 100.0%; Pred. No. 1.9e-90; Matches 184; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 184; Conservative
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; ORGANISM: Homo sapiens
US-10-216-074-11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-363A-27
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US-10-216-074-11
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US 60/214,591
PRIOR PILING DATE: 2000-06-27
PRIOR PLING DATE: 2000-06-12
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-06-12
PRIOR PILING DATE: 2000-06-12
PRIOR PILING DATE: 2000-06-12
SPRIOR PILING DATE: 2000-06-12
SOUTHARE: PACENTION NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-06-12
SOUTHARE: PACENTAIN NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-06-12
SOUTHARE: PACENTIN VERSION 3.1
SEQ ID NO 5
LENGTH: 181
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                                                                                                                    0; Indels
                                                           Score 950; DB 9; I
Pred. No. 5.1e-89;
                                     98.5%; scc...
100.0%; Pred. No. 5...
'... 0; Mismatches
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// Patent No. US20020081296A1
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 5, Application US/09855158; Publication No. US20020086018A1; GENERAL INFORMATION:
                                                     Query Match
Best Local Similarity 100.
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-09-855-158-5
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US-09-854-864-11
US-09-854-864-5
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                                                              ## APPLICANT: Markowitz, Sanford David
## APPLICANT: Markowitz, Sanford David
## APPLICANT: Markowitz, Sanford David
## APPLICANT: Bos Balotechnology, Inc.
## APPLICANT: Eso Balotechnology, Inc.
## APPLICANT: Case Western Reserve University
## APPLICANT: Case Western Reserve University
## TITLE OF INVENTION: Ociocate, Compositions and Methods of Screening for
## TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
## TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
## TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
## CURRENT APPLICATION NUMBER: US 60/272,206
## PRIOR PLILING DATE: 2001-04-02
## PRIOR PLILING DATE: 2001-04-02
## PRIOR PLILING DATE: 2001-04-02
## PRIOR PLILING DATE: 2001-04-07
## PRIOR PLILING DATE: 2001-04-07
## PRIOR PLILING DATE: 2001-04-07
## PRIOR PLILING DATE: 2001-04-17
## SOFTHARE: PATENTING DATE: 2001-04-17
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Patent No. US20020081296A1

GENERAL INFORMATION:

HIPPORMATION:

APPLICANT: THEILL, LARS EVDE

APPLICANT: TY, GANG

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B

CURRENT PILLING DATE: 2001-09-11

PRIOR PILLING DATE: 2000-09-12

PRIOR PILLING DATE: 2000-05-12

PRIOR FILLING DATE: 2000-06-12

PRIOR FILLING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin version 3.1

SEQ ID NO 5

LENGTH: 181
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OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
OTHER INFORMATION: 17 (TNFRSF17)
US-10-087-080-39
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
                                                                                              Search completed: February 26, 2005, 21:04:28 Job time : 140.37 secs
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Publication No. US20020086018A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EVDE
APPLICANT: THEILL, LARS EVDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
                          APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
FILTLE OF INVENTION: BLYS/AGP-3, AND TACI
FILTLE OF INVENTION: BLYS/AGP-3, AND TACI
FILTLE OF INVENTION: BLYS/AGP-3, AND TACI
FILTLE OF INVENTION: BLYS/AGP-3, AND TACI
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2010-09-11
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 11
LENGTH: 185
TYPE: PRI
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62.6%; Pred. No. 2.6e-50;
tive 21; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Indels
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         APPLICANT: THEILL, LARS EYDE
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Best Local Similarity 62.6*
Matches 117; Conservative
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US-09-855-158-11
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US-09-854-864-11
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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 26, 2005, 20:45:33; Search time 38.366 Seconds (without alignments) 461.448 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-077-438-1 964 1 MLQWAGQCSQNEYFDSLLHA......CKSLPAALSATEIEKSISAR 184

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
; Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	B-cell maturation	amino acid ABC tra	prominin - mouse	hypothetical prote	protein-tyrosine k	surface protein 51	protein R08F11.7 [protein-tyrosine k	furin (EC 3.4.21.7	potassium channel	killer cell inhibi	hypothetical prote		hypothetical prote	methyl-accepting c	hypothetical prote	hypothetical prote	ascites sialoglyco	complex I intermed	probable transcrip	hydrogenase chain	S-receptor kinase	ERD1 protein - yea	hypothetical prote	\circ	membrane protein [conserved hypothet	hypothetical prote	protein F20N2.12 [
SUMMARIES	QI	S43486	C97344	T08881	T13009	A57434	T28669	D89010	S60248	T43251	D64469	JC5894	D86345	T01733	T45824	F72288	T21152	T19277	A43353	T47250	T41478	B97297	A41369	S45592	T16840	JC7535	B95099	A97967	A89882	B96599
	DB	7	7	~	7	7	~	~	7	~	7	~	~	7	~	0	~	N	N	~	7	~	-	~	7	7	7	~	7	7
	Length	184	217	828	1998	1009	2233	773	1009	1299	343	841	738	968	522	539	357	1404	744	748	638	450	857	384	1101	377	307	307	304	619
dio	Query Match	100.0	9.5	9.0	8.7	8.5	8.5	8.4	8.2	8.2	8.1	. 8.1	8.0	8.0	8.0			7.9	•	٠	7.8	7.8	7.8	7.7	7.7	7.7	7.6	7.6	7.6	7.6
	Score	964	88.5	86.5	83.5	82	81.5		79.5	79.5	78.5	78	77.5	77.5	77	77	76.5	76.5	9/	94 .	75.5	75	75	74.5	74.5	74	73.5	73.5	73	73
	Result No.		7	m	4	S	9	7	80	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26		28	29

probable serine/th hypothetical prote	hypothetical prote hypothetical prote	hypothetical prote hypothetical prote conserved hypothet	probable cell divi ABC transporters (hypothetical prote spike glycoprotein	hypothetical prote hypothetical prote S-locus-specific g
A46373 T31144	S75097 T10665	T10350 B71709 F72334	G71331 AF1207	T10543 T02768	H82933 T24023 T14525
-100	100	200	000	00	000
733	416 855	105 627 227	414 473 480	200	188 412 424
7.6	2.7	4.4.4.	4.4.4	4.4	7.3
73.5	27.2	71.5	17 17	17.	70.5 70.5 70.5
31	1 W W C	3.5 3.7 3.7	3 8 8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4	4 4 4 6 4 0

ALIGNMENTS

1 11000	
S43486	4 10
B-cell	maturation factor - human
N;AIE	Nighternate names: BCM procein; BCMA procein; BEL procein
C; Date	c.ppcres. now, ompression and man., C.pate: 27dan-1995 #sequence revision 27-Jan-1995 #text_change 09-Jul-2004
C; Acce	ession: S43486; S31208; S36661
R; Laal	R.Laabi, Y.; Gras, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
A:Tit	ic Acids kes. 22, 114/-1154, 1994 le: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidir
A;Refe	number: S43486; MUID:94218235; PMID:8165126
A; Acce	A Accession: \$43.466
A; SCa(A/Sotatus: DIA A/NOJecuje type: DNA
A;Resi	A;Residues: 1-184 <laa></laa>
A, Croe	A;Cross-references: UNIPROT:Q02223; EMBL:Z29574; NID:g471244; PIDN:CAA82690.1; PID:g471
R; Laak	R.Laabi, Y.; Gras, W.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapls,
EMBC .	EMBG 0. 11, 389/-3504, 1992. B.T.H.tle. Brown care BRM on chromosome 16 is fineed to the interleukin 2 mone hv a t(4.
A;Refe	A;Reference number: S31208; MID:93010984; PMID:1396583
A; Acce	A;Accession: S31208
A; Mole	A, Molecule type: mRNA
A;Resi	A, Residues: 1-184 < LAZ>
A;Cros	A;CTOBS-TETECHOICES: EMBL:Z14954; NID:gZ940/; FIDN:CAA/86/9.1; FID:gZ9408
A; ACC	Ajaccession: socos. A. Ctatine, vivealiminary
A:Mole	Applemile type: mRNA
A;Resi	A; Residues: 4-184 <la3></la3>
A;Croe	A;Cross-references: EMBL:Z14955
C, Gene	CyGenetics:
A;Gene	Afgene: GDB:BUCKA A.Crea-rafevence. CDB:135977. OMIM:100545
A.Man	
A; Inti	A:Introns: 44/1: 93/1
C; Supe	C. Superfamily: human B-cell maturation factor
Que	100.0%;
Best	Best Local Similarity 100.0%; Pred. No. 4.1e-81; Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ò	1 MLOMAGOCSQUEYFDSLIHACIPCOLRCSSNTPPLITCORYCNASVINSVKGTNAILWICL 60
qa	1 MLQWAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
ò	61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
- 음	
λõ	121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
a	FPLP

F.; Sa

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A; Modecule type: mRNA
A; Residues: 1-1009 <SAS>
A; Residues: 1-1009 <SAS>
A; Cross-references: UNIPROT: P70600; GB: D45854; NID: 9100679; PIDN: BAA08290.1; PID: d10088.
C; Superfamaily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homoloo
C; Keywords: ATP; phosphotransferase; tyrosinae specific protein kinase
F; 423-686/Domain: protein kinase homology <KIN>
F; 431-439/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - rat
NyAlternate names: cell adhesion kinase-beta
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A57434
C;Accession: A57434
J; Biol. Chem. 270, 21206-21219, 1995
A;Title: Cloning and characterization of cell adhesion kinase beta, a novel protein-tyrony. A;Reference number: A57434; MUID:95403356; PMID:7673154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 71/3; 117/1; 162/3; 230/1; 309/3; 348/2; 396/1; 452/3; 532/2; 604/1; 1005/2; C;Superfamily: Arabidopsis thallana hypothetical protein T24C20.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Residues: 1-1998 <CHO>
A,Cross-references: UNIPROT:Q9STR8; EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20.80
A,Experimental source: cultivar Columbia; BAC clone T24C20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SSTGPFQDSEFENFSLGP 1122
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                                                                                                                                                                                                         219 FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 271
                                          | | | | | : : | | : : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                          ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 ORYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKD-EFKN--TGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1998;
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78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 82; DB 2;
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.7%; Score 83.5; DE 29.4%; Pred. No. 26; ative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1089 ERYCSA---NSALGTPSM---C-----
                                                                168 GFVANQOTRTRIKGTOK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.5%;
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272 LQDAATQLNTNLSS 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 29.4%
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                             ---SATEIEKSISA
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                                                                                                                                                                                                                                                                         Union acid ABC transporter, permease component CAC3619 [imported] - Clostridium acetobut C;Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97344
C;Accession: C97344
C;Accession: C97344
C;Accession: C97344
C;Accession: C97344
A;Reference number: A56900; MUD:21359325; PMID:21359325
A;Residues: 1-217.<KUR>
A;Residues: 1-217.<KUR>
A;Residues: 1-217.<KUR>
A;Coss-references: UNIPROT:Q97D61; GB:AE001437; PIDN:AAK81542.1; PID:g15026719; GSPDB:CA;Reperimental source: Clostridium acetobutylicum ATCC824
C;Genetion: Calcation of Comparation of Comparation of Comparation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation of Calcation 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 PLILQLYVXYYGLPFLSDKLTWTPMKAAILGLSLNSGAYIAEIIRGGILAIDNGOFBASK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---TCEDCI-KSKPKVDSDH 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 LHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
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Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SSLNKVIPVLLDGTRITLLLTCSSIIIGCIIGTIIAMFKTSSVKVLNLIGKFYTWILRGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Proc. Natl. Acad. Sci. U.S.A. 94, 12425-12430, 1997
A; Title: Prominin, a novel microvilli-specific polytopic memk
A; Reference number: Z16512; MUID:98024147; PMID:9356465
A; Accession: T08881
A; Scatus: preliminary; translated from GB/EMBL/DDBJ
A; Rolecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-858 <WEI>A; Cross-references: UNIPROT:054990; EMBL:AF0266269; NID:925590
A; Experimental source: Kidney
C; Keywords: glycoprotein; membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAVTPYLFAGIFYLILTTIFTGIFSK------IEKKLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 9.2%; Score 88.5; DB 2; Local Similarity 24.8%; Pred. No. 0.97; hes 55; Conservative 25; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: histidine permease protein M
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Best Local Similarity 22.,,
Local Similarity 22.,,
Annual 44; Conservative
                                                                                         181 ISAR 184
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R; Weigmann, A.; Cor
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Best Local Si
Matches 55,
            181
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C;Date: 10-Apr-1996 #sequence revision 27-Feb-1997 #text_change 16-Aug-2004
C;Accession: S60248; G02330; B57434
C;Accession: S60248; G02330; B57434
Nature 376, 737-745, 1995
A;Title: Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation of ion chan A;Reference number: S60248; MUID:95379967; PMID:7544443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1009 <LEV>
A;Cross-references: UNIPROT:Q14289; EMBL:U33284; NID:g988304; PIDN:AAC50203.1; PID:g988
R;Saaaki, T.; Nagura, K.; Sasaki, H.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01067
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A;Molecule type: mRNA
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: EMBL:043522; NID:91165218; PIDN:AAC05330.1; PID:91165219
R;Sasaki, H.; Nagura, K.; Ishino, M.; Tobioka, H.; Kotani, K.; Sasaki, T.
A;Molecule type: major type: mrna
A;Molecule type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type: mlocal type:
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A;Molecule type: mRNA
A;Residues: 1-22,'G',24-150 <SA2>
A;Cross-references: GB:D45853; NID:g1000676; PIDN:BAA08289.1; PID:d1008884; PID:g100067
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                                                                      184 PPKSNATCOGPPKSCSDPVHDRIRSITGYCNNRGKPTQANSVTAIRRLLGTTSYTDGLQA 243
                                                                                                                                            ISLAVFVLMFLLRKISSEPLKDEFKNTG-SGLLGMANIDLEKSRTGDEIILPRGLEYTV 123
                                                                                                                                                                                          244 IRNTSVTGSPLPSTRLISNKLHDEGSTPNFSPSVNHLHMQIGQFIAHDIIFMPSSTAKDG 303
                                                                                                                                                                                                                                                                                                                  304 SSINCTSC--SSPTTISTNCAPIPAPADDKYFTPVSRTEARCIRLTRALNGQSGFGVRTQ 361
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          -RYCN----ASVTNSVKGTNAILWTCL---GLSL
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C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;423-686/Domain: protein kinase homology «KIN»
F;431-439/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - human N;Alternate names: cell adhesion kinase-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
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llarity 32.1%; Pred. No. 31;
Conservative 9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                furin (EC 3.4.21.75) - fall armyworm
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              PCQLRCSSNTPPLTCQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N'Alternate names: cell adhes
C;Species: Homo sapiens (man)
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                                                                                                                                                                                                                                                                                                                                                                                                              177 IEKS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 IDON 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Rianonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUD1:99069613; PMID:9981916
A;Note: see websites genome.wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: D89910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Residues: Î-2233 «NIE»
A,Cross-referençes: UNIPROT:Q94711; EMBL:M65164; NID:g159974; PID:g159975; PIDN:AAA61740
C;Genetics:
A,Genetic code: SGC5
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                                                                         -----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
                                                                                                         562 TGSA------LIVKENCELKANREK---CGWTGSTCVDIVCTTAPTKTDD------D 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   520 GŚCYÓKQ------CSAASQDNTTHAQCQEYLPACTLSNTKKG------CIDLPL 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 IISLAVFVLMPLLRKISSEPLKDEFKNTGSGLLGMANIDL----EKSRTGDEIILPRGLE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Caenorhabditis elegans
C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 GOCSQNEYFDSLLHACIPCOLRCSSNTPPLTCORYCNA-SVTNSVKGTNAILWTCLGLSL
       Gaps
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       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
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                                                                                                                                                                                                                                            Length 2233;
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A;Map position: 5
C;Superfamily: myeloperoxidase; myeloperoxidase homology
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   34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Status: preliminary; translated from GB/EMBL/DDBJ; Molecule type: DNA
                                                                                                                                                                                                     DSDHCFPLPAME-----EGATILVTTKTND---
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8.5%; Score 81.5; DE
Best Local Similarity 25.1%; Pred. No. 45;
Matches 43; Conservative 17; Mismatches
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8.4%; Score 81; DB;
Best Local Similarity 21.7%; Pred. No. 17;
Matches 40; Conservative 25; Mismatches
   Mismatches
   13;
                                                               EFKNTGSGLLGMANIDLEKSR-
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C;Accession: JC5894
R;Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohy.
J; Biochem. 123, 358-368, 1998
A;Title: Genomic structures and chromosomal location of p91, a novel murine regulatory ?
A;Reference number: JC5894; MUID:98218758; PMID:9538215
A;Accession: JC5894
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-841 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT:Q8R2Z1; GB:AF040946
C,Comment: This protein function as inhibitory cell-surface molecule against cell activr
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;1-23/Domain: signal sequence #status predicted <SIG>
;4-841/Product: killer cell inhibitory receptor p91A #status predicted <WAT>
;24-18,119-220,221-315,316-418,419-517,518-619/Domain: extracellular Ig-like #status ;
;656-674/Domain: transmembrane #status predicted <TVM>
;675-765/Domain: cytoplasmic #status predicted <CYT>
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Ciho, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408; 816-820, 2000
A;Authors: Hunger, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: A86141; MUD:21016719; PMID:11130712
A;Residues: Drellminary
A;Molecule type: DNA
A;Residues: 1-738 <STO>
A;Residues: 1-738 <STO>
A;Residues: 1-738 <STO>
A;Residues: 1-738 <STO>
A;Residues: 1-738 <STO>
A;Residues: 1-738 <STO>
A;Cross-references: UNIPROT:091MN6; GB:AE005172; NID:g8920639; PIDN:AAF81361.1; GSPDB:GA.C;Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Species: Mus musculus (house mouse)
;Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 SQNEYFDSLLHACIPCOLRCS----SNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 IISLAVFVLMFLL--RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRG----
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                                                                                                                                                                                                                                              cell inhibitory receptor p91A precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | :||: | :||: | 700 RPNPAAATQEESLYASVEDMQTEDGVELNSWTPPEED-
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          ATILVTTKTND 163
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200 PNILITAKADE 210
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                            C;Species: Spodoptera frugiperda (fall armyworm)
C;Species: Spodoptera frugiperda (fall armyworm)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
B;Jan-2012 #separacterization of FURIN from Spodoptera frugiper
A;Reference number: 22236
A;Reference number: 22236
A;Reference number: 22236
A;Residues: 1-1299 cCIE>
A;Residues: 1-1299 cCIE>
A;Residues: 1-1299 cCIE>
A;Cross-references: UNIPROT:Q26489; EMBL:Z68888; NID:g1167859; PID:e219690; PIDN:CAA9311
A;Experimental source: clone Sfurin 6; ovary
C;Function:
A;Description: responsible for the endoproteolytic processing of proproteins with specif C;Reywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cyaccesion: D64469

K;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutron, G.G.; Blake, reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, M.G.; Merrick, J.M.; Glodek, A.; reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, M.G.; Merrick, J.M.; Glodek, A.; reon, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; Tile: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii A;Reference number: A64300; MUID: 96337999; PMID: 8688087

A;Reference pumber: A64300; MUID: 96337999; PMID: 8688087

A;Reference preliminary; nucleic acid sequence not shown; translation not shown
          serin
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   acid cleaving enzyme; proprotein convertase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : ::: | | | : | | | 1.206 GALHTAPSADAAPSVTIAVCAAAVGLFITVLVVVLQAHSPREKKTRKTSVRG----- 1259
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N/Alternate names: paired basic amino acid cleaving enzyme; proprotein conve
C,Species: Spodoptera frugiperda (fall armyworm)
C,Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
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Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
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A, Cross.references: UNIPROT:Q58752, GB:U67575, GB:L77:C;Genetics:
A, Map position: REV1308326-1307295
C, Superfamily: conserved hypothetical protein sll0993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         potassium channel homolog - Methanococcus jannaschii
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8.2%; Score 79.5; DE
Best Local Similarity 24.1%; Pred. No. 40;
Matches 39; Conservative 26; Mismatches
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Search completed: February 26, 2005, 21:05:24 Job time : 41.366 secs
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A;Map position: 1
C;Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25; prot
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A;Map position: 4
A;Introns: 112/3; 136/2; 164/3; 237/3; 356/1; 430/1; 460/2; 718/2; 752/3; 781/3; 806/3;
A;Note: A_IGO02N01.31
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C; Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C; Accession: T45824
R; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, January 2000
A; Reference number: Z23015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: T01733
A;Actus: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-968 <SCH>
A;Cross-references: UNIPROT:004623; EMBL:AF007269; NID:G2191126; PID:G2191152
A;Experimental source: cultivar Columbia
C;Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Peb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
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                                                                        Length 738;
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-522 cRIE>
A;Cross-references: UNTPROT:09M3B3; EMBL;AL132956
A;Experimental source: cultivar Columbia; BAC clone F2K15
                                                                                                                       45;
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                                                                        DB 2;
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A; Description: The sequence of A. thaliana IG002N01.
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A;Introns: 69/3; 271/3; 294/1; 327/3; 397/3; 443/3
A;Note: P2X15.50
                                                                     Query Match
8.0%; Score 77.5; DB
Best Local Similarity 26.2%; Pred. No. 34;
Matches 28; Conservative 21; Mismatches
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8.0%; Score 77.5; DE
Best Local Similarity 21.6%; Pred. No. 45;
Matches 35; Conservative 26; Mismatches
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methyl_accepting chemotaxis protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11.-un-1999 #sequence_revision 11.-Jun-1999 #text_change 09-Jul-2004
C;Accession: F72288
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se. A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72288
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A;Residues: 18-539 <ARN>
A;Cross-references: UNIPROT:Q9XONO; GB:AE001772; GB:AE000512; NID:g4981693; PIDN:AAD362
A;Cross-references: strain MSB8
C;Genetics:
A;Gene: TM1146
C;Superfamily: methyl-accepting chemotaxis protein
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C;Superfamily: Arabidopsis thaliana hypothetical protein F2K15.70
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                                                             Query Match 8.0%; Score 77; DB 2; Length 522; Best Local Similarity 27.0%; Pred. No. 27; Matches 27; Conservative 18; Mismatches 37; Indels
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203 --NVEIEKIRSKDEI 215
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Minimum DB Maximum DB

Database

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Result

Searched:

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SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
TISSUE=Lymph node, and Peripheral blood leukocytes;
MEDLINE=93010964; PubMed=139683;
Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,
Larsen C.J., Tsapis A.;
A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene
by a t(4;16) (q26;p13) translocation in a malignant T cell lymphoma.";
EMBO J. 11:3897-3904(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R., Larsen C.J., Tsapis A.;
during B lymphoid maturation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE FROM N.A.
MEDLINE=9425270; PubMed=10493829; DOI=10.1006/geno.1999.5927;
Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
Eichler E.B., Harris P.C., Venter J.C., Adams M.D.,
"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21419161; PubMed=11528522; DOI=10.1038/sj/gene/6363770; Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.; Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";
                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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25-OCT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor receptor superfamily member 17 (B-cell
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MEDLINE=94218235; PubMed=8165126;
Laabi Y., Gras M.P., Brouet J.C., Berger l.
Labi Y.A. gene, preferentially expressed (
is bidirectionally transcribed.";
Nucleic Acids Res. 22:1147-1154(1994);
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001820
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Q055773
Q18670
Q0802S1
T13X HUMAN
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DISEARS: Involved in a form of T-cell acute lymphoblastic leukemia DISEARS: Involved in a form of T-all) by a chromosomal translocation t(4;16) (q26;p13) which involves TWPRSF17 and IL2.
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Inoue J.-I., Devergen C., Tsaghs A.;
Inoue J.-I., Devergen C., Tsaghs A.;
Inoue J.-I., Devergen C., Tsaghs A.;
Inoue J.-I., Devergen C., Tsaghs A.;
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Inoue J.-I., Tsaghs A., Independent Branch C., Tsaghs A., Independent Branch Kinase, and p38 mitogen-activated protein kinase., J. Immunol. 165:1322-1330(2000).
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                                                                         FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3
                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 109545; -. Go. integral to membrane; TAS. GO:0016021; C:integral to membrane; TAS. GO:0004872; F:receptor activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 1 TNFR-Cys repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DIN: 543466; 543486.
PIR; 543466; 543486.
PDB; 10QD; X-ray; K/L/M/N/O/P/Q/R=8-46.
Genew; HGNC:11913; TNFRSF17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AB052772; BAB60895.1; -. AY509112; AAR84240.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   humoral immunity.";
Nat. Immunol. 1:252-256(2000).
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                                                                                                                                                                                                                                                   FUNCTION
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MEDILINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDILINE=22388277; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MIQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0007275; P:development; TAS.
GO; GO:0007165; P:signal transduction; TAS.
3D-structure; Chromosomal translocation; Immune response;
Polymorphism; Proto-oncogene; Receptor; Signal-anchor; Transmembrane.
DOMAIN 1 54 Signal-anchor for type III membrane
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                               Breakpoint for translocation to form IL2/TNFRSF17 oncogene.
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05-JJJ.-2004 (TrEMBLrel. 27, Last sequence update)
05-JJJ.-2004 (TrEMBLrel. 27, Last annotation update)
105-JJJ.-2004 (TrEMBLrel. 27, Last annotation update)
17-Jumor necrosis factor receptor superfamily, member 17.
                                                                                                                                                                   protein (Potential).
Cytoplasmic (Potential).
TNFR-Cys.
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/FTId=VAR_018755.
                                                                                                                                                                                                                                                                                                                                                                                                                       I -> V.
/FTId=VAR_018756.
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/FTId=VAR_018758.
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By similarity.
By similarity.
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Brownstein W.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glbbs R.A., Fahey J., Heltron E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A., Green E.D., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
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MEDLINE=99061155; PubMed=9846696;
MAGTY C. Leabi Y. Callebaut I., Roussel J., Hatzoglou A.,
Le Coniat M., Mornon J.P., Berger R., Tsapis A.;
"The characterization of murine BCMA gene defines it as a new member of the tumor necrosis factor receptor superfamily.";
Int. Immunol. 10:1693-1702(1998).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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STRAIN=CS7BL/6J; TISSUB=Colon;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC058291; AAH58291.1;
GO; GO:0004872; F:receptor activity; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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99.5%; Pred. No. 4.2e-81;
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Name=Tnfrsf17; Synonyms=BCM, BCMA;
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TISSUE=Pooled;
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Nikatado I., Omaru V. M. Saltor R., Suuthi H., Yamanada I., Kiyobaca H., Baddarali R., Momaru Y. M. Hasegawa Y., Nogami A., Schombach C., Golobori T., Baddarali R., Milli Dr., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C., Bull C.
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(See http://www.isb-sib.ch/announce/
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(BAFF-R) (BLyS receptor 3)
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EGUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
STRAIN=A/J;
MEDLINE=21475520; Pubmed=11591325; DOI=10.1016/S0960-9822(01)00481-X;
                                                                                                                                                                                                                                                                                                                                                                          4 MAGQCSQNEYFDSILHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                  LIISLAVFVLMFLLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        newly identified TNF receptor that specifically interacts
                                                                                                                                                                                                                                                                                                                                               Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
STRAIN-BALB/C; TISSUB-B-cell lymphoma;
MEDLINE-21442025; PubMed=11509692; DOI=10.1126/science.1061965;
Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
Cacheror T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
Ambrose C.;
                                                                                                                                                            membrane
                                        EMBL, AF061505, AAC23799.1; -.
EMBL, AK020247; BAB32038.1; -.
EMBL, BC027519; AAH27519.1; -.
HSSP, QO2223; LQQD.
MGD; MGI:1243050; Thfref17.
Alternative splicing; Immune response; Receptor; Signal-anchor;
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6
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                                                                                                                                         Extracellular (Potential).
Signal-anchor for type III me protein (Potential).
Cytoplasmic (Potential).
TNFR-Cys.
TNFR-Cys.
By similarity.
By similarity.
By similarity.
Missing (in isoform 2).
/FIIdaVSP_006507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
58-FEB-2004 (Rel. 44, Last annotation update)
55-JUL-2004. (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 13C activating factor receptor) (BAPF receptor) (BAPF-R) (E (B-cell maturation defect).
Name=Thfrsfl3c; Synonyms=Baffr, Bcmd, Br3;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                        8806352B4FD26A8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 AA
   entities requires a license agreement (St or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                           185 AA; 20442 MW;
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                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKSISAR 184
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                   Fransmembrane.
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with BAFF."
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TRANSMEM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                     KENDIBENCE KTOWN N.A. (1stOurwa 1).

SEQUIDENCE KTWORN N.A. (1stOurwa 1).

SECONDENCE KTWON N.A. (1stOurwa 1).

RA NIRAIN-CS7BL/63; PubMed=12466851; DOI=10.1038/nature01266;

RA OKazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondoo S.,

RA Nikaido I., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Nikaido I., Saito R., Bult C., Hume D.A., Quadchenbush J.,

RA Adarali R., Hill D.P., Bult C., Hume D.A., Quadchenbush J.,

RA Schriml L.M., Kanapin A., Matuda H., Eatalov S., Baisel K.W.,

RA Schriml I.M., Eradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

RA Gaasterland T.A., Pletcher C.F., Forrest A., Gough J.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Anai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Anai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Magoshima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Nagashima T., Numata K., Okido T., Raid J., Ringda K.,

RA Nagashima T., Numaka M., Pontulus J.U., Qi D., Ramachandran S.,

RA Sandelin A., Schneider C., Semple C.A., Setcu M., Sahada K.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells S.,

RA Nining L.G., Wynshaw-Boris A., Taylor M.S., Carninci P., Hayateu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hara A., Hashizume W., Imotani K., Itoh M., Kagawa I.,

RA Hara A., Hashizume W., Imotani K., Ishiada R.,

Rayanishi A., Yashina, Y.,

RA Hara A., Hashizume W., Waterston R., Lander E.S., Rogers J.,

Rayanishi A., Yashina, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isold=029BBD0-2; Sequence=VSP 006506;
Isold=09DBD0-2; Sequence=VSP 006506;
TISSUE SPECIFICITY: Highly expressed in spleen and testis;
detected at lower levels in lung and thymus.
DISEASE: Defects in Thirsfil3 are a cause of severe B-cell
deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb insertion
in the BAFFR gene leading to an altered C-terminus. The mutant RNA
is not detectable. B-cell lymphopolesis is normal, but the life
span of peripheral B-cells is much reduced.
SIMILARITY: Contains 1 TNFR-Cys repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21614654; PubMed=11747827; DOI=10.1016/S0960-9822(01)00598-X; Harless S. M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K., Hilbert D.M., Hayes C.E., Candro M.P.; Competition for BLyS-mediated signaling through Bcmd/BR3 regulates peripheral B lymphocyte numbers."; Curr. Biol. 11:1986-1989(2001).
-!- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLyS. Promotes the survival of mature B-cells and the B-cell response... SUBCELLULAR LOCATION: Type III membrane protein (Probable)...- ALTERRATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                            that
Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M., Canoro M.P., Grewal I.S., Dixit V.M.;
"Identification of a novel receptor for B lymphocyte stimulator is mutated in a mouse strain with severe B cell deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
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                                                                                                                 Curr. Biol. 11:1547-1552(2001).
                                                                                                                                              [3]
SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=2;
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EMBL; AF373847; AAK91827.1; -.

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TNR6 BC
P51867;
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                                 TNR6 BOVIN
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                                                                                                                                                                                                                                                                                                                                                           57 WTCLGLSLI--ISLAVFVLMFLLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111
                                                                                                                                                                                                                                                                                                                                                                             57 WTCLGLSLI--ISLAVFVLMFLLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111
                                                                                                                                                                                                                                                                                                   7 QGSQNEYFDSLLHACIPCQL-----RCSSNTPPLTCQRYCNASVTNSVK---GTNAIL 56
                                                                                                                                                                                                                                                                                                                      21 QCNQTECFDPLVRNCVSCELFHTPDTGHTSSLEPGTALQPQEGSALRPDVALLVGAPALL 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 QCNQTECFDPLVRNCVSCELFHTPDTGHTSSLEPGTALQPQEGSALRPDVALLVGAPALL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                      membrane
                                                                                                                                                    By similarity.
N-linked (GlcNAc. . .) (Potential).
Missing (in isoform 2).
/FTId=VSP_006506.
                                                                                                                                                                                                                                                                          35;
                                                                                                                                                                                                                                                                                                                                                                                                                                   -:--PHASAPTWPPLK-EDADSALPR----HSVPVPATELGSTELVITKT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----PHASAPTWPPLK-EDADSALPR----HSVPVPATELGSTELVTTKT 170
                                                                                                                                                                                                                                                                                                                                                                                                                  112 BIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKT 161
              HSSP; 096RJ3; 100E.
MGD; MGI:1919299; Tnfrafl3c.
Alternative splicing; Glycoprotein; Immune response; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.1%; Score 116.5; DB 2; Length 175; 29.4%; Pred. No. 0.0091; Live 21; Mismatches 64; Indels 35.
                                                                                                                                                                                                                                              DB 1; Length 175;
                                                                                                                                                                                                                                                                          64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mizuno K., Irie S., Sato T.-A.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF1360257; AAL83914.1; -.
HSSP, 905RJ3; 199299; Thfref13c.
GO; GO:0016021; C:integral to membrane; TAS.
SEQUENCE 175 AA; 18846 MW; B64EFF4B52EE93B1 CRC64;
                                                                        Extracellular (Potential).
Signal-anchor for type III
                                                                                                 protein (Potential).
Cytoplasmic (Potential).
TNFR-Cys (incomplete).
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                           12.1%; Score 116.5; DB 1
29.4%; Pred. No. 0.0091;
tive 21; Mismatches 6'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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EMBL; AK008142; BAB25490.1; -.
                                                                                                                                                                                                                  175 AA; 18798 MW;
                                                          Signal-anchor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2003 (TrEMBLrel. 24,
TRARF3 binding protein.
Name=Tnfrsfl3c;
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Les 50; Conservative
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21
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133
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DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                     VARSPLIC
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                                                                                                                                                                                                                                                                                         MEDLINE=96226401; PubMed=8634151;
Yoo J., Stone R.T., Beattie C.W.;
"Cloning and characterization of the bovine Fas.";
"Cloning and characterization of the bovine Fas.";
"Cloning and characterization of the bovine Fas.";
"L. DNA Cell Biol. 15:227-234(1956).
"Cloning and characterization of the activated receptor. The resulting deathing recruits cappase-8 to the activated receptor. The resulting deathinducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (sapartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral colerance, in the amy have a role in the induction of peripheral colerance, in the samidantique similarity).

C.I. SUBCELLULAR LOCATION: Type I membrane protein.

C.I. SUBCELLULAR LOCATION: Type I membrane protein.

C.I. DOMAIN: Contains a death domain involved in the binding of FADD, and maybe to other cytosolic adaptor proteins.

C.I. SIMILARITY: Contains 3 INFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R InterPro; IPR000488; Death.
R InterPro; IPR011029; DEATH like.
R InterPro; IPR011029; DEATH like.
R InterPro; IPR011029; Pag = receptor.
R InterPro; IPR011029; Tag = receptor.
R Pfam; PF00020; Tag = receptor.
R Pfam; PF00020; Tag = receptor.
R SMART; SM00005; DEATH; 1.
R SMART; SM00005; DEATH; 1.
R PROSITE; PS50017; DEATH DOWAIN; 1.
R PROSITE; PS50017; DEATH DOWAIN; 1.
R PROSITE; PS50050; Tark NGFR 2; 2.
R Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
I SIGNAL
I 10 323 Thmor necrosis factor receptor
                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2096 (Rel. 45, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
(CD95 antigen).
Name=TNFRSF6, Synonyms=APT1, FAS;
                                                                                                                                                            Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             superfamily member 6.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoplasmic (Potential).
TNFR-Cys 1.
TNFR-Cys 2.
TNFR-Cys 3.
 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Death.
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential
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188
323
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1163
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                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           NCBI_TaxID=9913;
                                                                                                                                                                                                                    Bovinae; Bos
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BOVIN
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셤
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                                                                                                                                                                                                                                                                                                                                                 CSEGNEYTDKSHHSDKCIRCSICDEEHGLEVEQNCTRTRNTKCRCKSNFFCNSSPCEHCN 141
                                                                                                                                                                                                                                                                                                                                                                                                               KDEFKNTGSG-----LLGMANIDL-----EKSRTGD--EIILPRGLEYTVEECTCED 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLTCQ----RYCNASVTNSVKGTNA---ILWTCLGLSLIISLAVFVLMFLLRKISSEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M., Cancro M.P., Grewal I.S., Dixit V.M.;

"Identification of a novel receptor for B lymphocyte stimulator that is mutated in a mouse strain with severe B cell deficiency.";

-ur. Biol. 11:1547-1552 (2001).

-ir FUNCTION: B-cell receptor specific for THFSF13B/TALLI/BAFF/BLyS.

-promotes the survival of mature B-cells and the B-cell response.

-ir SUBCELLULAR LOCATION: Type III membrane protein (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21475520; Pubmed=11591325; DOI=10.1016/S0960-9822(01)00481-X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a newly identified TNF receptor that specifically interacts
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-COT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor receptor superfamily member 13C (B cellactivating factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
No similarity.
By similarity.
Whinked (GlCNAc. . .) (Potential).
Whinked (GlCNAc. . .) (Potential).
Why 4D88A90E9E1F4892 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIKSKPKVDSDHCFPLPAMEEGATILVT----TKTNDYC---KSLPAALS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : |: | || || || || || 254 IMH----ETARQKVQLLRNWYQSHGKKNAYCTLTKSLPKALA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB-B-cell lymphoma;
MEDLINE=21442025; PubMed=11509692; DOI=10.1126/science.1061965;
Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
Cachero T.G., Hession C., Schneider P., Slzing I.D., Mullen C.,
Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
                                                                                                                                                                                                                                                                    82;
                                                                                                                                                                                                                                                                                                          8 CSQ-NEYFDSLLHA--CIPCQL------RCSSN----
                                                                                                                                                                                                                         DB 1; Length 323;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                              22.1%; Pred. No. 2.1; ive 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 AA
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                                                                                                                                                                                                                             9.8%; Score 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=TNFRSF13C; Synonyms=BAFFR, BR3;
                                                                                                                                                                                         36445 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 293:2108-2111(2001).
                                                                                                                                                                                                                                                                      Conservative
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  79
1116
1124
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    60
82
101
1104
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143
143
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323 AA;
                                                                                                                                                                                                                                                 Local Similarity
nes 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ambrose C.;
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with BAFF.
                       DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                           33
                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78
             Note=No experimental confirmation available, TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and in resting B-calls. Detected at lower levels in activated B-calls, resting CD4+ T-cells, in thymus and peripheral blood leukocytes. SIMILARITY: Contains 1 TNFR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 W---TCLGLSLIISLAVFVLMF-----LLRKISSEPLKDEFKNTGSGLLGMANIDLEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 RIGDEIILPRGLEYTVEECTC-----EDCIKSKPKVDSDHCFPLPAMEEGATILVTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALOPQESVGAGAGEAALPLPGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSQNEYFDSLLHACIPCQL------RCSSNTP--PLTCQRYCNASVTNSVKGTNAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PSO0652; TWFR NGFR 1; FALSE NEG.
PROSITE; PSS0050; TWFR NGFR 2; FALSE NEG.
3D-structure; Alternative splicing; Immune response; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal-anchor for type III protein (Potential). Cytoplasmic (Potential). INFR-Cys (incomplete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F2BFB98099A27138 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             By similarity.

By similarity.

P -> PA (in isoform 2).

/FIId=VSP_006505.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.6%; Score 93; DB : 26.5%; Pred. No. 1.5; tive 20; Mismatches
Isold=096RJ3-2; Sequence=VSP_006505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=pedC;
symbiont bacterium of Paederus fuscipes
                                                                                                                                                                                                                                                                                                                                                            100E; X-ray; K/L/M/N/O/P/Q/R=16-46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18863 MW;
                                                                                                                                                                                                                                                                                                                    EMBL; AF373846; AAK91826.1; -. PDB; 1MPV; NMR; A=23-35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:17755; TNFRSF13C.
MIM; 606269; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal-anchor; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Putative acyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
99
                                                                                                                                                                                                                                                                                                                                                                                         10SX; NMR; A=1-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=176282;
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SEQUENCE FROM N.A.
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18
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143
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InterPro; IPR009030; Grow_fac_recept
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               InterPro; IPR006210; IEGF.
SMART; SM00181; EGF; 22.
SMART; SM00261; FU; 29.
                                                                                                                                                                 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1488;
                                                                                                                                                                                                                                                      42
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Q97D61
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                                                                                                                                                                                                                                                                                                                                                                                                                                               70 VFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 THVENILFNLIKQARLFDEYCNAGAMLLVIDHID------TFSTTPAFSK 164
                                                                                                                                                                                                                                                                                                                                                                                    14 FÖSLLHACIPCOLRCSSNTPPLTCORYCNAS--VTNSVKGTNAILWTCLGLSLIISLA-- 69
                                                                                                 PubMed=14973122; DOI=10.1128/JB.186.5.1280-1286.2004;
Piel J., Hofer I., Hui D.;
Piel J., Hofer I., Hui D.;
Piel J., Hofer I., Hui D.;
Piel J., Hofer I., Hui D.;
Piel J., Hofer I., Hui D.;
Piel J., Hofer I., Hui D.;
Piel J., Horizontal acquisition of pederin biosynthetic capabilities by the bacterial symbiont of Paederus figscipes beetles.";
J. Bacteriol. 186:1280-1286(2004).
EMBL; AY328023; AA847559.1;
CO; GO:0008415; P:acyltransferase activity; IEA.
GO; GO:0016740; P:transferase activity; IEA.
GO; GO:001872; P:metabolism; IEA.
InterPro; IPR001227; Ac_transferase.
Pfam; PP00689; Acyl_transf. 1; 1.
                                                                                                                                                                                                                                                                                                                                                          39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Stock d4-2;
PubMed=15296759; DOI=10.1016/j.cub.2004.07.029;
Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,
Gromadda R., Noel B. And I., Dessen P., Wincker P., Keller A.M.,
Cohen J., Meyer B., Sperling L.,
"High Coding Density on the Largest Paramecium tetraurelia Somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative surface protein with EGF domains and furin-like repeats.
ORFNames=PTMB.409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paramecium tetraurelia.
Eukaryota: Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                           "A polyketide synthase-peptide synthetase gene cluster from an uncultured bacterial symbiont of Paederus beetles.";
Proc. Natl. Acad. Sci. U.S.A. 99:14002-14007(2002).
MEDLINE=22294974; PubMed=12381784; DOI=10.1073/pnas.222481399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 DCIKSKPKVDSDHCFPLPAMEEGATILVT----TKTNDYCKSLPAALS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DC--ELAGINFDHCFVVSGPRTG--ILOTRKSLTKQNIACQLLPVSIA 208
                                                                                                                                                                                                                                                                                                                             Length 334;
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Nowak J. V., Migdalski A., Gromadka R., Zagulski M.;
Nowak J. V., Migdalski A., Gromadka R., Zagulski M.;
Natamecium megabase sequencing project.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR548612; CAH03606.1;
InterPro; IPR00056; 2F22_fd BS.
InterPro; IPR000345; Cytc heme BS.
InterPro; IPR0005209; EGF_like.
                                                                                                                                                                                                                                                                                                334 AA; 38018 MW; 6C42D1FFEC5E35F3 CRC64;
                                                                                                                                                                                                                                                                                                                          Query Match 9.6%; Score 92.5; DB 2; Best Local Similarity 25.0%; Pred. No. 3; Matches 42; Conservative 22; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 3005 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006212; FurIn_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Curr. Biol. 14:1397-1404(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paramecium.
NCBI_TaxID=5888;
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                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 DEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVE-----ECTCEDCIKSKPKV-- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1314 CESIHLRSFNNSNKC---PCLDGYFDVGIEMCQKCNDLCKTCQSISTQCLSCYETEQ 1367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----NASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPL----K
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-!- SUBILARITY: Belongs to the binding-protein-dependent transport system permease family.
--- SIMILARITY: Belongs to the binding-protein-dependent transport by the permease family.

EMBL; AB007858; AAK81542.1; ---
PIR; C97344; C97344.

G0; G0:0016021; Cintegral to membrane; IEA.

G0; G0:0016021; Cintegral to membrane; IEA.

G0; G0:0005215; F:transports activity; IEA.

InterPro; IPR0000515; BD_transport; IEA.

InterPro; IPR0000515; BD_transport.

InterPro; IPR0000519; IRGO ABC_3TM.

Pfam; PF00528; BDD_transp_1; 1.
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLOMAGOC-SQNEYFDSLLHACIPCQLRCSSNTPPLTCQ---RYC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Mismatches 59; Indels 104;
                                                                                                                                                                                                                                                                                                                                 Query Match 9.2%; Score 89; DB 2; Length 3005; Best Local Similarity 20.3%; Pred. No. 63;
PROSITE; PS00197; 2FE2S_FERREDOXIN; UNKNOWN_1.
PROSITE; PS00199; CYTOCHOWNE_C; UNKNOWN_2.
PROSITE; PS001186; EGF_2; 12.
SEQUENCE 3005 AA; 343821 MW; D8CC6A247876A5A5 CRC64;
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SEQUENCE 217 AA; 23743 MW; 36738BCDC0DE8A2F CRC64;
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Last sequence update)
Last annotation update)
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PROSITE; PSS0928; ABC_TM1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the membrane (By similarity).
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10;
                                                                                                                                                                                                                                                                                                63 SLIISLAVFV--LMFLLRKISSEPLKDEF----KNTGS------GLLGMANIDLEKSR 108
                                                                                                                                                                                                                                                                                                                                                                                      ------TGDEIILPRGLEYTVEEC------TCEDCI-KSKPKVDSDH 142
                                                                                                                                                                                                                                                                                                                                                                                                                                 163 GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLLTETPKQIDYVVEQYTNTKNKA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 FSDLDGIGSVLGGRIKDQLKFKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE--- 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of novel Prominin-1/CD133 splice variants with alternative C-termini and their expression in epididymis and testis."; J. Cell Sci. 117:4301-4311(2004).

SMED: AX223521; AA072429.1; -. MGD; MG1:1100886; Proml.

GO; GO:0005903; C:brush border; IDA.

GO; GO:0005902; C:microvillus; IDA.

GO; GO:0005902; C:microvillus; IDA.
                                                                                                                                                                         | |: || | : | || || SSLNKVIPVLLDGTRITLLTTCSSIIIGCIIGTIIAMFKTSSVKVLNLIGKFYTWILRGT
                                                                                                                             16 SLIHACIPCOLRCSSNTPPLTCQRYCNASV-----TNSVKGTNAI----LWTCLGL
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fargeas C.A., Joester A., Missol-Kolka E., Hellwig A., Huttner W.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                     65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53;
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      Length 217;
                                                                  77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 CFPLPAMEEGA - TILVTTKTNDYCKSLPAALSATEIEKSIS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----iEKKLS 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
      DB 2;
                                       4.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               804 AA
9.2%; Score 88.5; D
24.8%; Pred. No. 4.6;
tive 25; Mismatches
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PubMed=15316084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004, (TrEMBLrel. 26, Prominin-1 T2 isoform.
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267 LQDAATQLNTNLSS 280
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les 44; Conservative
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                    Best Local Similarity
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      Query Match
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Matches
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080XB3
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130 ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Identification of novel Prominin-1/CD133 splice variants with alternative C-termini and their expression in epididymis and testis."; J. Cell Sci. 117:4301-4311 (2004).
EMBL; AY223522; AAO72430.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 GFVANQQTRITRIKGTQK-----LAKSNFRDFQTLLITTPKQIDYVVEQYINIKNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 LHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Testis;
PubMed=15316084;
Farges C.A., Joester A., Missol-Kolka E., Hellwig A., Huttner W.B.,
Corbell D.;
"Identification of novel Prominin-1/CD133 splice variants with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fargeas C.A., Joester A., Missol-Kolka E., Hellwig A., Huttner W.B.,
Corbeil D.;
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Prominin T4 isoform.
Name=Promoyns=Prom;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musines; Mus
                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
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GO; GO:0005903; C:brush border; IDA.
GO; GO:0005807; C:integral to plasma membrane; IDA.
GO; GO:0005902; C:microvillus; IDA.
Interbro; IRR008795; Prominin.
Pfam; PP05478; Prominin; 1.
SEQUENCE 809 AA; 90605 MW; BC99IE100C623AE1 CRC64;
                                                                                                                          Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                809 AA
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STRAIN-BALB/c; TISSUE~Testis;
PubMed=15316084;
                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26, Prominin-1 m? 4-4-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
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272 LQDAATQLNTNLSS 285
                                                                PRELIMINARY;
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                                                                                                                                                                                                                    Prominin-1 T3 isoform.
                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                 Name=Prom1;
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Q80XB6;
                                                                Q80XB2
RESULT 12
Q80XB2
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H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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Matches 44; Conserv
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                                                                                                                                                                                                                  RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE--- 129
                                                                                                                                                                                                                                                                                                         ----DCIKS-----KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
                                                                                                                                                                                                                                                                                                                         219 FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 271
                                                                                                                                                                                                  18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
  expression in epididymis and testis.";
                                                                                                                                                                                                                                                                    168 GPVANQQTRIRIKGTQK------LAKSNFRDFQTLLTETPKQIDYVVEQYINTKNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Hutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4931440N24 product:prominin, full insert sequence.
Name=Prom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                         53;
                                                                                                                                               DB 2; Length 823;
                                                                                                                                                                        67; Indels
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SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Testis;
MEDLINE-21085660; PubMed=11217851; DOI=10.1038/35055500;
                                     MGD; MGI:1100886; Proml.
GO; GO:0005903; C:brush border; IDA.
GO; GO:0005903; C:bruseral to plasma membrane; IDA.
GO; GO:0005902; C:microvillus; IDA.
InterPro; IRRO08795; Prominin.
Pfam; PFO5478; Prominin; I.
SEQUENCE 623 AA; 92225 MW; 9EF01A18DB84EFAC CRC64;
                                                                                                                                            Query Match
9.0%; Score 86.5; DB
Best Local Similarity 22.7%; Pred. No. 28;
Matches 44;; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
alternative C-termini and their es
J. Cell Sci. 117:4301-4311(2004).
EMBL, AY099088; AAM28245.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE=Testis;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                             :||:: ::|:
272 LGDAATQLNTNLSS 285
                                                                                                                                                                                                                                                                                                                                                            ---SATEIEKSISA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Hukuda S., Furuno M., Hanaqaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Inotani K., Ishii Y., Itoh M., Kagawa I., Kauda M.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,
Nahi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Oksato N.,
Saito R., Saitoh H., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,
Tagawa A., Takahashi P., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databasee.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVBECTCE---- 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
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                                                                                                                                                              SEQUENCE FROM N.A.

C STRAIN=C57BL/6J; TISSUB=Testis;

MEDLINE=C55BL/6J; TISSUB=Testis;

MEDLINE=C55BL/6J; TISSUB=Testis;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakagudi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Prominin T1 isoform (Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932416E19 product:prominin, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF05478; Prominin; 1.
renirance 827 AA; 92714 MW; DBCA5ED2DF401A18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1100886; Promi.
GO; GO:0005903; C:brush border; IDA.
GO; GO:0005887; C:integral to plasma membrane; IDA.
GO; GO:0005902; C:microrallus; IDA.
InterPro; IPR008795; Prominin.
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272 LQDAATQLNTNLSS 285
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(JUL-2001) to the EMBL/GenBank/DDBJ databases.

Submitted

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                                                                                                                                                                                                                  "Identification of novel Prominin-1/CD133 splice variants with. alternative C-termini and their expression in epididymis and testis."; J. Cell Sci. 117:4301-4311(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL/6J; TISSUB=Testis; MEDLIRE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLIRE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nuramatsu M., Hayashizaki Y.; Pubbraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayatawa I., Hiroka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kaukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sakai C., Sakai K., Shinagawa A., Takahashi F., Tagami M., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                          STRAIN=CS-BL/6J; TISSUB=Testis; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; High-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Testis;
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Min = 10. Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunato H., Sakaguchi S., Ikegami T., Kashiiwaji K., Fuliwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rike integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                             Fargeas C.A., Joester A., Missol-Kolka E., Hellwig A., Huttner W.B.
                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=CSTBL/60; TISSUE=Testis;
MEDLINE=2108560; Pubmed=11217851; DOI=10.1038/35055500;
RIKEN FANYOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUE=Testis;
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STRAIN=C57BL/6J; TISSUE=Testis;
                                                                                                                                           STRAIN=BALB/c; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 409:685-690(2001).
                    Mus musculus (Mouse)
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                                                                           NCBI_TaxID=10090;
                                                                                                                                                            PubMed=15316084;
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117 LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 GFVANQQTRIRIKGTQK-----LAKSNFRDFQTLLTETPKQIDYVVEQYINTKNKA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
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                                                                                                                                                                                                                                                                                                                                                                 18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL
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                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                  53,
                                                                                                                                                                                                                                                                  Length 834;
                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                   Ffam; PF05478; Prominin; 1.
SEQUENCE 834 AA; 93444 MW; 5ABA26C80F636E45 CRC64;
EMBL; AF305215; AA011840.1; -...
EMBL; AK030027; BAC26745.1; -...
MGD; MG11100886; Prom1.
GO; GO:00058903; C:brush border; IDA.
GO; GO:0005887; C:integral to plasma membrane; IDA.
GO; GO:0005902; C:microvillus; IDA.
                                                                                                                                                                                                                                                                                                                  67;
                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                               30; Mismatches
                                                                                                                                                                                                                                                             9.0%; Score 86.5; I 22.7%; Pred. No. 28;
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                                                                                                                                                                                                                                                                                                                    44; Conservative
                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                               Matches
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Search completed: February 26, 2005, 21:00:48 Job time : 178.953 secs

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5.1.6
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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OM protein - protein search, using sw model

February 26, 2005, 20:45:33 ; Search time 10.634 Seconds (without alignments) 461.448 Million cell updates/sec Run on:

US-10-077-438-1_COPY_1_51
283
1 ML@MAGQCSQNEYFDSLLHA.....TPPLTCQRYCNASVTNSVKG 51 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is defived by analysis of the total score distribution.

Result No.		% Query Match	% Query Match Length	DB	SUMMARIES	Description
-	283	100.0	184	~	S43486	B-cell maturation
0	70.5	24.9	1548	~	S34583	serine proteinase
m	69.5	24.6	5376	~	T42215	zonadhesin - mouse
4	68.5	24.2	1101	7	T16840	al
Ŋ	65.5	23.1	1299	~	T43251	4
9	62.5	22.1	666	~	T19275	hypothetical prote
7	62	21.9	330	7	T25169	
8	61.5	21.7	66	~	860231	н
0	61.5	21.7	483	N	T24856	hypothetical prote
10	61.5	21.7	520	N	G88846	
11	0	21.4	1574	7	T13954	MEGF6 protein - ra
12	60.5	21.4	3034	~	T14119	seven-pass transme
13	59.5	21.0	388	N	T31887	hypothetical prote
14	59.5	21.0	388	~	T31888	
15	59.5	21.0	438	N	T31889	
16	59.5	21.0	445	~	T31898	
17	59	20.8	758	~	T15577	a
18	59	20.8	1717	ч	A45558	U
19	58.5	20.7	2533	~	T28675	alpha-51D immobili
20	58.5	20.7	2533	~	T28674	alpha-51D-immobili
21	28	20.5	63	~	S07127	chymotrypsin/elast
22	28	。	1513	N	T23681	hypothetical prote
23	58		1816	٦	096898	laminin alpha-4 ch
24	57.5	20.3	1680	~	A43434	furin (EC 3.4.21.7
25	57	20.1	502	N	T20130	hypothetical prote
56	57	20.1	653	~	G96675	_
27	57	20.1	838	~	T20125	_
28	56.5	20.0	701	~	862460	
29	26	19.8	2476	N	T34022	zonadhesin - pig

hypothetical prote	cathepsin B (EC 3.	protein R09F10.7 {	S-receptor kinase	hypothetical prote	hypothetical prote	cathepsin B (EC 3.	finger protein YJL	hypothetical prote	hypothetical prote	vascular endotheli	membrane glycoprot	hypothetical prote	membrane protein y	hypothetical prote	alpha tectorin - m
T22759	KHRTB	B89588	T05754	T01519	T23682	KHIMSB	S46625	T27283	T27303	869207	JC5486	C90879	H64888	G85739	T30197
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13	13	19	19	19	13	13	13	13	13	13	19	19	13	19	19
26	55.5	55.5	55.5	55.5	55	22	55	22	54.5	54.5	54.5	54.5	54.5	54.5	54.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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RESULT 1
S44366
B-cell maturation factor - human
Nalternee names: BCM protein; BCMA protein; BEL protein
C;Species: Homo sapiens (man)
C;Accession: S44366; S31208; S36661
R;Heabl, Y; Gras, M.P.; Brouer, U.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nalternees: BCMA gene, preferentially expressed during B lymphoid maturation, is bidir.
R;Heabl, Y; Gras, M.P.; Brouer, U.C.; Berger, R.; Larsen, C.J.; Tsapis, A.;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidir.
A;Reference number: S4436; MUID:94218235; PMID:8165126
A;Retus: prefilminary
A;Nolecule type: DNA
A;Residues: 1-184 <LAA
A;Cross-references: UNTROT:Q02223; EMBL:229574; NID:9471244; PIDN:CAA82690.1; PID:9471
A;Residues: 1-184 <LAA
A;Residues: 1-184 <LAA
A;Residues: 1-184 <LAA
A;Residues: 1-184 <LAA
A;Reference number: S31208; MUID:93010984; PMID:1396583
A;Recession: S31208
A;Recession: S31661
A;Retus: preliminary
A;Rolecule type: mRNA
A;Retus: preliminary
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A;Retus: preliminary
A;Rolecule type: mRNA
A;Cross-references: EMBL:214955
C;Generics
A;Gene: Colse-references: GDB:135977; OMIM:109545
A;Rolecule type: MLD: 16p13.1
A;Introns: 4441; 9314
C;Superfamily: human B-cell maturation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1
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Gapa . 0 Length 184; Indels Query Match 100.0%; Score 283; DB 2; Best Local Similarity 100.0%; Pred. No. 8.6e-25; Matches 51; Conservative 0; Mismatches 0;

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51 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG

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RESULT 2 S34583 임

serine proteinase (EC 3.4.21.-) PC6B - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004 C;Accession: S34583 R;Nakagawa, T.; Murakami, K.; Nakayama, K.

5.2;

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Best Local Similarity
Matches 17; Conserv
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My Gao, L. 2., Garbers, D.L.

J. Biol. Chem. 273, 3415-3421, 1998

A; Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane pro

A; Reference number: Z22080; MUID: 98123114; PMID: 9452463

A; Accession: T42215

A; Residual profilminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA

A; Residuals: 1-5376 cGAo>

A; Cross-references: UNIPROT:088799; EMBL:U97068; NID:93327420; PID:93327421; PIDN:AAC266

C; Genetics: A; Gene: San

A; Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical profein T10E10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16840
R;Geisel, C.
submitted to the EMBL Data Library, October 1995
R;Geisel, C.
submitted to the EMBL Data Library, October 1995
A;Reseasion: T16840
A;Recession: T16840
A;Recession: T16840
A;Recession: T16840
A;Recession: T16840
A;Recession: T16840
A;Recession: T16840
A;Recidues: J-1101 < GEI>
A;Residues: J-1101 < GEI>
A;Residues: J-1101 < GEI>
A;Residues: L-1101 < GEI>
A;Residues: L-1101 < GEI>
A;Recession: T16810.4
A;Recession: T16810.4
A;Residues: CESP:T10E10.4
                                                                                                                                    A,Molecule type: mRNA
A,Residues: 1-1548 <NAK>
A,Residues: 1-1548 <NAK>
A,Cross-references: UNIPROT:004592; GB:D17583; NID:g407344; PIDN:BAA04507.1; PID:d100503
C,Keywords: hydrolase; serine proteinase
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A;Introne: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3;
FBBS Lett. 327, 165-171, 1993
A;Title: Identification of an isoform with an extremely large Cys-rich region of PC6,
A;Reference number: S34583; MUID:93327934; PMID:8335106
                                                                                                                                                                                                                                                                                                                                           ٦;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        7 OCSONBYFDSLLHACIPCOLRCSSNTPP----LICORYCNASVTNSVK 50
                                                                                                                                                                                                                                                                                  Length 1548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 5376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: functions in multiple cell adhesion processes A; Note: found exclusively on the apical region of the sperm head C; Keywords: cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3299 QCPTNSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC 3336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 OCSONEYFDSLLHACIP-COLRCSSNTP--PLTCORYC 41
                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: sperm-specific membrane protein
                                                                                                                                                                                                                                                                         Query Match

24.9%; Score 70.5; DB
Best Local Similarity 34.7%; Pred. No. 4.1;
Matches 17; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Match 24.6%; Score 69.5; D
Local Similarity 36.8%; Pred. No. 15;
les 14; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68.5;
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                                                                                  A; Accession: S34583
A; Status: preliminary
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Matches
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furin (EC 3.4.21.75) - fall armyworm
NyAlternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
Syspecies: Species: Species: Species: Species: Species: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43251
Sk;Cieplik, M.; Klenk, H.
submitted to the EMBL Data Library, January 1996
A;Description: Cloning and functional characterization of FURIN from Spodoptera frugipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reaidues: 111299 <CIB>
A;Cross-references: UNIPROT:Q26489; EMBL:Z68888; NID:g1167859; PID:e219690; PIDN:CAA9311:
A;Experimental source: clone Sfurin 6; ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C'Function:
A,Description: responsible for the endoproteolytic processing of proproteins with specif
C,Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q17969; EMBL:Z37139; PIDN:CAA85494.1; GSPDB:GN00021; CESP:F3:
A;Experimental source: clone C14B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Introns: 20/3; 40/3; 72/1; 234/3; 387/3; 457/1; 523/2; 541/3; 682/1; 784/2; 822/2; 870
                                                             'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F34D10.2 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T19275; T21723
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1299;
                                                                                                                                            350 QCSQSTVFNSDLAVCVPLAIQNSCDSSTQQPVCS--C-SQVSSSCPG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 999;
                                                                                                                 51
                                                                                                              7 QCSQNEYFDSLLHACIPCQLR--CSSNTPPLTCQRYCNASVTNSVKG
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
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                                                       15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T43251
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rikershaw, J.
submitted to the EMBL Data Library, June 1994
A;Reference number: 219464
A;Accession: T21723
A;Accession: T21723
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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34.0%; Pred. No. 13;
tive 8; Mismatches
                           Pred. No. 5.2;
); Mismatches
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42.5%; Pred. No. 23;
tive 2; Mismatches
36.2%; Etc. 10;
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Best Local Similarity 34.0%
Matches 18; Conservative
                                                   17; Conservative
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Matches 17; Conservative
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A; Residues: 1-999 <WIL>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Essidues: 1-483 <WIL>
A;Cross-references: UNIPROT:Q22423; EMBL:Z73911; PIDN:CAA98142.2; GSPDB:GN00022; CESP:T
A;Experimental source: clone T12A7
A;Experimental source: clone T12A7
A;Gene:CESP:T12A7.2
A;Map position: 4
A;Introns: 36/3; 71/1; 146/1; 255/2; 287/2; 340/3; 387/1; 449/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo. A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_el A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an A;Accession: G88846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q22423; GB:chr_IV; PIDN:CAA98142.1; PID:g3879789; GSPDB:GNO:C;Genetics:
A;Gene: T12A7.2
A;Map position: 4
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C;Date: 20-Sep.1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Date: 20-Sep.1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13954
B;Nakayama, M: Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: Z14126; MUID:98360089; PMID:9693030
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A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein T12A7.2 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G88846 F. Sequencing Consortium.
Science 282, 2012-2018, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                  5;
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                                                                                                                                                                                                                                                                                                                                           Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 CMNDGYFNHTLGRCV----CTSNWVGEHCIFRCNSGVVNKTSG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 CMNDGYFNHTLGRCV----CTSNWVGEHCIFRCNSGVVNKTSG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
21.7%; Score 61.5; DE
Best Local Similarity 31.8%; Pred. No. 17;
Matches 14; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                    Query Match
21.7%; Score 61.5; I
Best Local Similarity 31.8%; Pred. No. 16;
Matches 14; Conservative 5; Mismatches
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21.4%;
Best Local Similarity 32.2%;
Matches 19; Conservative
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A, Residues: 1-520 <STO>
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            A; Accession: T24856
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A;Molecule type: DNA
A;Residues: 1-330 <MIL>
A;Residues: 1-330 <MIL>
A;Cross-references: UNIPROT:018118; EMBL:281129; PIDN:CAB03405.1; GSPDB:GN00023; CESP:TZ
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.Herzog, M.; Dórne, A.M.; Grellet, F.
Plant Mol. Biol: 27, 743-752, 1995
A:Title: GASA, a glbberellin-regulated gene family from Arabidopsis thaliana related to A:Title: GASA, a glbberellin-regulated gene family from Arabidopsis thaliana related to A:Title: GASA, a glbberellin-regulated gene family from Arabidopsis thaliana related to A:Totession: S6d231
A:Status: nucleic acid sequence not shown
A:Status: nucleic acid sequence not shown
A:Status: nucleic acid sequence not shown
A:Status: 1-99 cHER.
A:Cross-references: UNIPROT:P46687; EMBL:U11764; NID:g887934; PIDN:AAB06308.1; PID:g8879
C;Generics:
A:Gene: GASA3
C;Generics:
A:Gene: GASA3
C;Superfamily: glbberellin-regulated protein GASA2
F;1-18/Domain: signal sequence #status predicted <MAT>
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                                                                                                                                                                              C'Species: Caendrhabditis elegans
C'Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
C'Accession: T29169
R;Wilkinson, J
Submitted to the EMBL Data Library, October 1996
A;Reference number: 219990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gibberellin-regulated protein GASA3 precursor - Arabidopsis thaliana N;Alternate names: GAST1 protein homolog C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: 09-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T12A7.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24856
R;Lennard, N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 CASSQOYQLQTSQCMPACQQSCSQQCQSNTNTQCQPTCQQSCQTSSCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Indels
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516 YEDSLLKTCIGRAFERVKKMTPPLRIQSYFVSSTPNGLDG 555
                                                                                                                                                   hypothetical protein T23F1.6 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 62; DB 2
Pred. No. 10;
7; Mismatches
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Best Local Similarity 35.6%; Pred. No. 4.2;
Matches 16; Conservative 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 21.9%;
Best Local Similarity 29.2%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: CESP:T23F1.6
A,Map position: 5
A,Introns: 16/3
C,Superfamily: gliadin
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R;Greco, T.; Bradshaw, H.; Elliott, G.
submitted to the RMEL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C03A7.
A;Reference number: Z21096
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31.9%;
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Best Local Similarity 31.9%;
Matches 15; Conservative
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Best Local Similarity 31.9
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A; Introns: 75/3
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A; Introns: 75/3
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C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 22-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C; Accession: T31887
R; Greco, T.; Bradshaw, H.; Elliott, G.
submitted to the EMBL Data Library, July 1997
A; Reference number: 221096
A; Reference number: 221096
A; Reterence number: 221096
A; Residues: Tallinary; translated from GB/EMBL/DDBJ
A; Residues: 1-388 GRE>
A; Residues: 1-388 GRE>
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A; Residues: 1-388 GRE>
A; Residues: 1-38
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K;Hadjantonakis, A.K.; Formstone, C.J.; Little, P.F.R.
submitted to the EMBL Data Library, October 1997
A;Description: The Celsr family of novel evolutionarily conserved seven-pass transmembra
A;Reference number: 217881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3034 <HAD>
A;Cross-references: UNIPROT:035161; EMBL;AF031572; NID:g3800735; PID:g3800736; PIDN:AACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Map position: 15,
C.Keywords: transmembrane protein
C.Keywords: transmembrane protein
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-3034/Product: seven-pass transmembrane receptor protein #status predicted <MAT>
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                                             7 QCSQNEYFDSLLHACIPCQL-----RCSSNTPPLTCQ-----RYCN-----ASVTN 47
        ---NASVTNSVKG 51
                                                                                                                                                                                                                                                                  seven pass transmembrane receptor protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 QCAPQCEQS-------CQQQCVQQQQPAQCQTACQSSCSNS 350
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Best Local Similarity 31.9%;
Matches 15; Conservative
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A,Map position: 6
A,Introns: 75/3
C;Superfamily: gliadin
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T31888
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hypothetical protein CO3A7.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C;Accession: T31888

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A,Residues: 1-438 <GRE>
A,Cross-references: UNIPROT:O16502, EMBL:AF016451, PIDN:AAB65995.1, GSPDB:GN00023, CESP:
A,Experimental source: strain Bristol N2; clone C03A7
                                                                               A; Cross-references: UNIPROT:O16501; EMBL:AP016451; PIDN:AAB65996.1; GSPDB:GN00023; CESP. A; Experimental source: strain Bristol N2; clone C03A7 C; Genetics:
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C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31889
R;Greco, T; Bradshaw, H.; Elliott, G.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C03A7.
A;Reference mumber: Z21096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 QCAPQCEQS------CQQQCVQQQQPAAQCQTACQSSCSNS 350
                                                                                                                                                                                                                                                                                                                    Length 388;
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A,Accession: T31888
A,Status: preliminary: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-388 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: T31889
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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Pred. No. 25;
4; Mismatches
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Pred. No. 22;
4; Mismatches
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TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 6, Appli
Sequence 5, Appli
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Sequence 18110, A
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                                                                                                                                 February 26, 2005, 20:57:04; Search time 13.0213 Seconds (without alignments) 292.376 Million cell updates/sec
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Sequence 21,
Sequence 7, A
Sequence 13,
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Sequence 11,
Sequence 10,
Sequence 12,
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Sequence 22
Sequence 4,
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3. /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

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5. /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
5.1.6
Compugen Ltd.
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US-09-854-864-16
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Sequence 41037, A	Sequence 56253, A	Sequence 4, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 6, Appli	7	316	-	Sequence 11, Appl	Sequence 2, Appli	Sequence 10932, A	Sequence 9, Appli		Sequence 41714, A	Sequence 11984, A	Sequence 12, Appl	Sequence 10, Appl
US-09-270-767-41037	US-09-270-767-56253	US-09-561-818A-4	US-09-561-818A-8	US-09-561-818A-2	US-09-561-818A-6	US-09-848-295-2	US-09-270-767-31650	US-09-270-767-46867	US-09-589-892B-11	US-08-276-967-2	US-09-949-016-10932	US-08-718-388-9	US-09-270-767-56958	US-09-270-767-41714	US-09-902-540-11984	US-09-561-818A-12	US-09-561-818A-10
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20.7	20.7	20.5	20.5	20.5	20.5	20.3	20.1	20.1	20.1	19.8	19.6	19.6	19.4	19.4	19.4	19.4	19.4
58.5	58.5	58	28	58	58	57.5	57	57	57	26	55.5	55.5	52	52	55	55	52
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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US-09-854-864-21

i Sequence 21, Application US/09854864

j Patent No. 6774106

j GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EXDE

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR PILING DATE: 2000-06-27

NUMBER OF SEO ID NOS: 31

SEO ID NO 2:

LENGTH: 58

LENGTH: 58
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09854864
Petent No. 6774106
GENERAL INFORMATION
GENERAL INFORMATION:
TOTAL OF INVERTION METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVERTION: BLYS/AGP-3, AND TACI
FILE REFRENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT PAPLICATION NUMBER: US 60/204,039
PRIOR FLING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 48
                                                                                                                                                           4 MAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
                 Score 269; DB 4; Length 181;
Pred. No. 1.5e-24;
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Pred. No. 1.1e-22;
95.1%; scc...
100.0%; Pred. No. 1...
0; Mismatches
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1 Similarity 100.0%; Pred. No. 2.5
48; Conservative 0; Mismatches
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ive 0, Mismatches
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Best Local Similarity 100.0
Matches 48; Conservative
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Matches 44; Conservative
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ORGANISM: Homo sapiens
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US-09-854-864-21
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Best Local Similarity
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLXS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR PILING DATE: 2000-05-12
PRIOR PLILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 6
LENGTH: 51
LENGTH: 51
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TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: METHODS AND TACI
FILE REPERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT PELING DATE: 2001-09-11
PRIOR FILING DATE: 2000-06-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PALENTING DATE: 2000-06-27
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                                                                                                                                                                                                                                                Query Match 100.0%; Score 283; DB 4; Length 192; Best Local Similarity 100.0%; Pred. No. 3.5e-26; Matches 51; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 11115
LENGTH: 192
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Patent No. 6774106
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Patent No. 6774106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.0
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-09-854-864-5
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                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                US-09-949-016-11115
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Length 283;

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Gaps

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Length 58;

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Sequence 11, Application US/09854864

Sequence 11, Application US/09854864

Batent No. 6774106

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

TITLE OF INVENTION:

FILE REFERENCE: A-686E

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR PILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE PARENTIN VERSION 3.1

SOFTWARE PARENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US/04,039
             TITLE OF INVENTION: TALL'I NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 4.5e-14;
4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 185;
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Pred. No. 4.5e-14;
4; Mismatches 8;
                           CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: UNKNOWN
PRIOR APPLICATION NUMBER: UNKNOWN
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
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                                                                                                                                                                                                                                                                                                                                                                                         64.0%;
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Best Local Similarity 70.8°
Matches 34; Conservative
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Shu, Hong-Bing
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-565-423-17
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Best Local Similarity
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: TYU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTHARE: PATENTIN Version 3.1
                                                                                                                   GENERAL INFORMATION:
APPLICANT: THEILL, LARS EXDE
APPLICANT: THEILL, LARS EXDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATCHIN VETSION 3.1
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100.0%; Pred. No. 3.1e-17;
tive 0; Mismatches 0;
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100.0%; Pred. No. ...
... 0; Mismatches
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Patent No. 6475987
GENERAL INFORMATION:
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Sequence 13, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
                                                                            Sequence 7, Application US/09854864
Patent No. 6774106
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Best Local Similarity 100.0
Matches 34; Conservative
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Best Local Similarity 100.(
Matches 34; Conservative
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US-09-854-864-7
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LENGTH: 81
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Length 59; Indels

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23.9%; Score 67.5; DB 4; 30.6%; Pred. No. 0.41; tive 9; Mismatches 15;
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                                                                                                                                                                                                   RESULT 14
US-08-810-572A-6
US-08-810-572A-6
; Sequence 6, Application US/08810572A
; Patent No. 5963102
; GENERAL INFORMATION:
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Best Local Similarity 30.6%;
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amino acid
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                                                                                      Query Match 23.9
Best Local Similarity 30.6
Matches 11; Conservative
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                          ; ORGANISM: Homo sapiens
US-09-854-864-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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MOLECULE TYPE:
HYPOTHETICAL: 1
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US-09-290-333-6
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        TYPE: PRT
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TEGLIL, LARS EYDE
APPLICANT: TEGLIL, LARS EYDE
APPLICANT: TYU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US 09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
36.7%; Score 104; DB 4; Length 117;
Best Local Similarity 69.8%; Pred. No. 3.9e-05;
Matches 30; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                        4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCORYCNASVTNSVKG
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                                                                                                                                                                                                                                      Score 181; DB 4;
Pred. No. 7e-14;
                                                                                                                                                                                                                                                                            4, Mismatches
PRIOR FILING DATE: 2000-05-12
PRIOR PEDLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 10
LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09854864
Patent No. 6774106
GENERAL INFORMATION:
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Patent No. 6774106
GENERAL INFORMATION:
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Best Local Similarity 70.8%;
Matches 34; Conservative
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SEQ ID NO 12
LENGTH: 117
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US-09-854-864-10
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APPLICANT: Bram, Richard J.
APPLICANT: WON Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SUBFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                     ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A FILING DATE: 28-FEB-1997 CLASSIFICATION: 536
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Pred. No. 1.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 28-FEB-1997
CLASSIFTCATION: 536
ATTORNEY/AGENT INFORMATION:
NAWE: Jackson Bsq., David A.
REGISTRATION NUMBER: 26,742
REPRENCE/DOCKET NUMBER: 1340-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 6, Application US/09290333
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von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
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                                                                                                                                                                                                                         CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZUP: 07601

COMPUTER: ESADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OHERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN FC-L099
CURRENT APPLICATION NUMBER: US/09/290,333
FILING DATE: 1-2-Apr-1999
CURRENT APPLICATION NUMBER: 26,742
ATTORNSY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION INFORMATION:
TELEPHONE: 201-497-5800
TELEPHONE: 201-497-5800
TELEPHONE: 201-497-5800
TELEPHONE: 201-497-5800
TELEPHONE: 201-497-1684
INFORMATION:FOR ESQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acide
TYPE: amino acid
STYPE: amino acid
STYPE: amino acid
STYPE: mino acid
STYPE: mino acid
STYPE: Deptide
HYPOTHEITCAL: NO
FRAGENISM: Homo sapiens
CONTGINAL SOURCE:
ONGANISM: Homo sapiens
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23.9%; Score 67.5; DB 3; Length 166;
Best Local Similarity 30.6%; Pred. No. 1.2;
Matches 11; Conservative 9; Mismatches 15; Indels
                                                                                                                                                    NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNA 43
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                                             APPLICANT: Bram, Richard J.
; Patent No. 6316222
; GENERAL INFORMATION:
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Search completed: February 26, 2005, 21:06:29
Job time : 14.0213 secs

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The present sequence represents a BCMA (not defined) polypeptide. BCMA is a necrosis factor (NF)-kB activator. The method of the invention is used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a recombinant anti-cell death gene and a reporter gene operably linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene
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283
1 MLQMAGQCSQNEYFDSLLHA.....TPPLTCQRYCNASVTNSVKG
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                                                                                       2005, 20:24:52
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Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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AAE09241
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Gapop 10.0 , Gapext 0.5
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geneseqp2000s:*
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geneseqp2004s:*
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length: 2000000000
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Human BCM
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ALIGNMENTS

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BCMA, necrosis factor-kB activator, NF-kB; gene expression, cancer, anti-cell death gene; apoptosis, viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; septic shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57. .77 /note= "putative transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
AAB08843 standard; peptide; 184 AA
                                                                                                                                                                                             Amino acid sequence of human
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the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NP-kB expression and thus for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; BR41X2; TACI receptor; extracellular domain; BCMA; B cell protein; transmembrane activator and CAML-interactor; tumour necrosis factor; TNF; ztnf4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematoeus; mysthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vaculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a human BCMA protein, a B cell protein related to transmembrane activator and CAML-interactor (TACI) receptor. TACI is a tumour necrosis factor (TNP) receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell protein) receptor contain a cysteine rich domain, and are used for inhibiting ztnf4 activity. ZhAI is a TNF ligand. They may also be used for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
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                                                                                                                                                                                                                                                                                                                                                                        1 MLQMAGQCSQNBYFDSLLHACIPCQRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                          100.0%; Score 283; DB 3; Length 184; 100.0%; Pred. No. 1.2e-25; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A human BCMA protein, a B cell protein related to TACI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 152; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY94001 standard; protein; 184 AA.
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                                                                                                                                                                                                                                                                           Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-452538/39.
                                                                                                                                                                                                                  Sequence 184 AA;
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                                                                                                                                                                            designing
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with activated or resting B lymphocytes, effector T-cells, or with autibody production. The antibody production is associated with an autibody production is associated with an autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The zinf4 activity and BR43x2, TAGI or BCWA receptor-ligand engagement is associated with asthma, bronchitis, emphysema, end stage renal failure, renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy, amploidosis, moderating immune response, immunosuppression, graft rejection, graft versus host disease, inflammation, insulin dependent diabetes mellitus, Crohn's disease, inflammation, insulin dependent septic shock. BR43x2, TAGI, and BCMA polypeptides, fusions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery stenosis, or occlusion, and cholesterol or renal emboli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to methods of using one or more agonists or matagonists to modulate the activity of the members of TNF (tunnour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions of diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 KRCI or BCMA. They are useful for treating between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; TNF; tumour necrosis factor; TALL-1; APRLL; TNF receptor; TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma; autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pitti RM;
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
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                                                                                                                                                                                                                                                                                                                                                                                                                          1 MLOMAGQCSQNEYFDSLLHACIPCOLRCSSNTPPLITCORYCNASVTNSVKG
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                                                                                                                                                                                                                                                                                                                                               Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                           Match 100.0%; Score 283; DB 3; Local Similarity 100.0%; Pred. No. 1.2e-25; les 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE09241 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 2; 160pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-FEB-2000; 2000US-0182938P.
22-AUG-2000; 2000US-0226986P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-541628/60.
N-PSDB; AAD15902.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human BCMA protein.
                                                                                                                                                                                                                                                                                                        Sequence 184 AA;
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myasthenia gravis, Grave's disease, autoimmune haemolytic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thompson J;
      sclerosis,
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                                                                                                                                                                                                                                                                                                                                                          AAB60698;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for regulating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid archiritis, systemic lupus erythematosus (SLE), insulin dependent diabetes mellitus, multiple
                                                                                                                                                                                                                                                                                                                                        Human; Tumdur Necrosis Factor; TNF; immunosuppressant; TALL-1; Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus; thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome; haemolytic ansemia; Grave's diseas; myssthenia gravis; chromosome 16; post-streptococcal glomerulonephitis; polyarteritis nodosa; BCMA; B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention relates to Tumour necrosis factor (TNF) and Apol-
a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, pacariasis and lupus erythematosus. The present sequence is human BCMA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated TALL-1 protein is used to identify compounds that regulate B lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders.
                                                                                                                      Gaps
                                                                                                                                             1 MLOMAGQCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
                                                                                                                                                          1 MLQWAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                                                                            Length 184;
                                                                                                                    Indels
                                                                                         100.0%; Score 283; DB 4; 100.0%; Pred. No. 1.2e-25;
                                                                                                                                                                                                                                                                                                                 Human B cell maturation factor (BCMA) protein.

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    /label= Extracellular_domain

                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                  AAY71979 standard; protein; 184
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                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                    Conservative
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                                                                                                       Similarity
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                                                                 Sequence 184 AA;
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                                                                                                                   51;
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Best Local S:
Matches 51,
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anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, penebabiga vulgaris, acute rheumatic fever, post-streppococcal glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays. The present sequence is a human B cell maturation factor (BCMA) protein. It is the receptor for TALL-1 protein. BCMA gene is located on chromosome 16. In human tissues, BCMA is expressed by spleen and lymph nodes but not BCMA manages. BCMA is expressed by spleen and lymph nodes but not BCMA manages with B lymphocyte stage but its expression increases with B lymphocyte maturation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune-related disorder; B-cell growth inhibitor; BCMA; B-cell maturation inhibitor; mamunoglobulin production inhibitor; autoimmuned disorder; B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 283; DB 4; 100.0%; Pred. No. 1.2e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB60698 standard; protein; 184 AA
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11-FEB-2000; 2000US-0181684P.
18-FEB-2000; 2000US-0183536P.
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Claim 3; Fig 3A; 85pp; English.

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the TNF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF.R, fusion proteins containing it, and BAFF.R. specific antibodies can be used for inhibiting B-cell growth, dendritic, cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders. B-cell lymphoproliferative disorders, hypertension and renal disorders. B-cell lymphoproliferative clusters, hypertension and renal disorders and HIV be used in the treatment of immunosuppressive disorders and HIV proteins or BAFF-R specific antibodies may be used for treating, cuppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, grave's disease, multiple mayeloma, B-cell carcinomas, leukaemia, rapidly progressive glomerulonepiritis, and lymphomas. Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents human BAFF-R
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Sequence 184 AA;

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                                                                                   1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                           1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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tch 100.0%; Score 283; DB 4; Length 184; sal Similarity 100.0%; Pred. No. 1.2e-25; 51; Conservative 0; Mismatches 0; Indels (
                     Best Local Similarity
    Query Match
                                         Matches
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Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic; gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; acationom; Lung; colon; breaat; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease; B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF; tumour necrosis factor; BCMA; B cell maturation protein. Human B cell maturation protein (BCMA). AAE00506 standard, protein; 184 AA (first entry) 31-JUL-2001 AAE00506; AAE00506 RESULT HAT HAT YELD YOU WANTE

WO200124811-A1. Homo sapiens.

12-APR-2001

05-OCT-2000; 2000WO-US027579

06-OCT-1999; 99US-0157933P. 11-FEB-2000; 2000US-0181807P. 30-JUN-2000; 2000US-0215688P.

(APOT-) APOTECH R & D SA. (BIOJ) BIOGEN INC.

Rennert P; Cachero T, Ambrose C, Schneider P, Thompson J,

WPI; 2001-266242/27. N-PSDB; AAD03844. Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) antagonist

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cassociated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A proliferation inducing ligand Receptor (APRIL-R) also referred as B cell maturation protein (BCM or BCMA) antagonist that antagonists the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or carcinoma e.g. human lung carcinoma, once arcinoma, breast carcinoma, prostate carcinoma, and other carcinoma whose proliferation is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's diseases, renal disorders, B-cell lympho-proliferative disorders, ciseases, renal disorders, B-cell lympho-proliferative disorders.

Immunosuppressive diseases, organ transplantation, inflammation and human immune response involving a signalling pathway between APRIL-R DNA is also useful in gene therapy. The present sequence
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                                                                      The invention relates to a method of treating a mammal for a condition
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 283; DB 4; Length 184; 100.0%; Pred. No. 1.2e-25; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is human APRIL-R also referred as BCMA or BCM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 184 AA;
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1 MLQWAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51 ABB81487 standard; protein; 184 AA RESULT 7 ABB81487 셤

1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51

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ABB81487;

02-SEP-2002 (first entry)

Human BCMA receptor related protein SEQ ID NO:7.

immunosuppressive; dermatological; antiinflammatory; antidiabetic; neuroprotective; antirheumatic; antiarthritic; antiasthmatic; nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthma; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; gylomenulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis; pyelonephritis; amyloidosis; inchitish chain neuropathy; hypertension; large vessel disease; graft-versus host disease; graft rejection; Crohn's disease. Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;

WO200238766-A2.

16-MAY-2002.

05-NOV-2001; 2001WO-US047018.

07-NOV-2000; 2000US-0246449P. 20-DEC-2000; 2000US-0257131P. 28-UUX-2001; 2001US-0301715P. 29-AUG-2001; 2001US-0315565P.

(ZYMO) ZYMOGENETICS INC.

Grant FJ; Gross JA, Xu W, Henne RM,

WPI; 2002-508212/54.

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The present interaction describes a numan tumour necrosary receptor designated Zthfri2 (I). (I) has cytostatic, immunosuppressive, dermatological, antinflammatory, neuroprotective, antidathritic, antiarthritic, antiarthritic, entracthritic, antidathriatic, nephrotropic and hypotensive activities, and can be used in gene therapy. (I) can be used for inhibiting, in a mammal, the activity of a ligand that binds Zthfri2 (e.g. ZTNR4), for treating disorders and diseases associated with B (minibiting the proliferation of tumour cells. (I) is useful for treating inhibiting the proliferation of tumour cells. (I) is useful for treating cutoimmune disorders such as systemic lupus erythematosis, myasthenia C artoimune disorders such as systemic lupus erythematosis, asthma, creutamune disorders such as systemic lupus erythematosis, myasthenia C gravis, multiple sclerosis, inpulin dependent diabetes mellitus, asthma, creumatosid arthritis, bronchitis, emphysema and end stage renal failure C reumandidisease such as glomerulomephritis, vasculitis, chronic lymphoid leukaemia, nephritis, and pyelonephritis, and for treating renal c neoplasms, multiple myelomas, lymphonas, light chain neuropathy, or amyloidosis, hypertension, large vessel diseases, graft-versus host disease, graft rejection and Crohn's disease. (I) is useful for modulating the immune system, for regulating B cell responses and development, for modulating development of other cells, antibody production, and cytokine production, and for modulating T and B cell communication. The present sequence represents a protein which is given in the exemplification of the present invention
Novel isoldted human tumor necrosis factor receptor polypeptide, termed Stnfr 12, useful for treating autoimmune disorders, emphysema, end stage renal failure or renal disease and lymphoma.
                                                                                                                                        invention describes a human tumour necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metastasis; differential expression; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MICOMAGQCSQNEYFDSLLHACIPCQRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 283; DB 5; Length 184; 100.0%; Pred. No. 1.2e-25; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metastatic colorectal cancer-associated polypeptide.
                                                                                           Disclosure; Page 135-136; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP54694 standard; protein; 184 AA.
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UNIV CASE WESTERN RESERVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colorectal cancer; metastasis; didiagnosis; gene therapy; vaccine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 184 AA;
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The present sequence is the protein sequence of a human polypeptide encoded by a gene that exhibits decreased expression in colon cancerderived metastages compared to normal colon tissue. It is an example of claimed polypeptides that are encoded by genes which are differentially expressed in metastatic colorectal cancer cells. Such polypeptides are useful in diagnostic and prognostic assays, for raising antibodies useful e.g. in immunotherapy, and in screening for modulator compounds of
     for
New genes that are up- or down-regulated in colorectal cancer, useful for diagnosing colorectal cancer in a subject, or for identifying modulators of colorectal cancer-associated proteins and genes for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; tumour; B-cell maturation antigen; transmembrane activator; calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy; neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease; non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                MLÓMAGOCSONEY FDSLLHACI PCOLRCSSNTPPLTCORYCNASVTNSVKG
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                                                                                                                                                                                                                                                                                               Length 184;
                                                                                                                                                                                                                                                                                             100.0%; Score 283; DB 5; Length 1 100.0%; Pred. No. 1.2e-25; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Antigenic epitope"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human B-cell maturation antigen (BCMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE28961 standard; protein; 184 AA
                                                                                 Claim 8; Page 255; 260pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 51, Conservative
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                                                  colorectal cancer.
                                                                                                                                                                                                                                  therapeutic value
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                                                                                                                                                                                                                                                                Sequence 184 AA;
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The invention relates to the manufacture of a composition for inhibiting the proliferation of tumour cells. The method involves using an antibody component that binds both the B-cell maturation antigen (BCMA) and the transmembrane activator and calcium-modulator and cyclophilin ligandinteractor (TACI). BCWA and TACI binding antibody compositions are useful for inhibiting proliferation of tumour cells, particularly inhibiting ZUNF4 activity in a mammal associated with increased endogenous antibody production or a disorder consisting of neoplasm, chronic lymphocytic leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation lymphoproliferative disease or light chain gammopathy or inflammation e.g. asthma. The invention is also useful in gene therapy. The present is
Disclosure; Page 63; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                             human BCMA protein
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Sequence 184 AA;

ö Gaps ; 0 Length 184; Indels ch 100.0%; Score 283; DB 5; Similarity 100.0%; Pred. No. 1.2e-25; 51; Conservative 0; Mismatches 0; Query Match Best Local S Matches

21 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG

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AAE35216 standard; protein; 184

AAE35216;

Human B-cell maturation receptor (BCMA) protein. 28-MAY-2003 (first entry)

Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin; anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive; glomerulonephritis; asthma; bronchitis; graft rejection; septic shock; dermatological; neuroprotective; cyclophilin ligand-interactor; human; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation; B-cell maturation receptor; BCMA; receptor.

Homo sapiens.

WO200294852-A2

28-NOV-2002

20-MAY-2002; 2002WO-US015910.

24-MAY-2001; 2001US-0293343P.

(ZYMO) ZYMOGENETICS INC

Gross JA; Rixon MW,

WPI; 2003-148455/14. N-PSDB; AAD53754. Transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI)-immunoglobulin fusion protein, for treating cancer or diabetes, comprises a TACI receptor group and an immunoglobulin group.

Disclosure; Col 100; 71pp; English.

The invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumour necrosis factor-like protein (ZTNF) or ZTNF4; and an immunoglobulin group comprising a constant region of an immunoglobulin. The invention is used to manufacture a medicament for

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological activity in mammal, has a modification in the region connecting beta strands D and E that reduces the biological activity of TALL-1
                   composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic inpus erythematosus, multiple sclerosis, diabetes mellitus, rheumatoid arthritis and acthma), renal diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft rejection, anaemia and septic shock. The fusion proteins are also used gene therapy. The present sequence is human B-cell maturation receptor (BCMA) protein used in the invention
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory; antiarthritis; dermatological; antidiabetis; neuroprotective; antithyroid; antipyretis; nephrotropis; vasotropis; vaccine; autoimmune disease; rheumatoid arthriti; systemic lupus erythematosus; insulin dependent diabetes mellitus; multiple sclerosis; myasthaenia gravis; Grave's disease; autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura; Goodpasture's syndrome; pemphigus vulgaris; acute rheumatic fever; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.
 inhibiting the proliferation of tumour cells in a mammalian subject.
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                                                                                                                                                                                                             Length 184;
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                                                                                                                                                                                                           100.0%; Score 283; DB 6;
100.0%; Pred. No. 1.2e-25;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                     ADA49361 standard; protein; 184 AA
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14-JAN-2002; 2002US-0348962P.
07-FEB-2002; 2002US-0354966P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human BCMA protein.
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                       Sequence 184 AA;
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dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic, nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in a vaccine. A protein of the invention is useful for inhibiting TALL-1 biological activity in a mammal TC is useful for treating autoimmune diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin dependent diabetes mellitus, multiple sclerosis, myasthaenia gravis, carave's disease, autoimmune hemolytic anaemia, autoimmune thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis and polyarteritis nodosa. The present sequence represents human BCMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel antibody or its fragment, which immunospecifically binds tumour necrosis factor Delta (TNP-delta/ARRIL). The antibody of the invention has dermatological, immunosuppressive, antiinflammatory, antirheumic, antiarthritic, cytostatic, antianaemic, antiallergic, antiabetic, antiportective, ophthalmological, tuberculostatic, antiabetic, antiporiatic, anti-HTV, antiarteriosclerotic, vasotropic, thyronimetic, and haemostatic activity. The antibody or its fragment are useful for treating, preventing or ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVHD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APRIL; scFv; immunospecific; tumour necrosis factor delta; TNF-delta; dermatological; immunosuppressive; antiinflammatory; antirheumatic; antiantritic; cytostatic; antianemnic; antiallergic; antiallergic; neuroprotective; ophthalmological; tuberculostatic; antidiabetic; antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic; antipsoriatic; anti-FIV; antiarteriosclerotic; vasotropic; thyromimetic; hammatory disorder; proliferative disorder; single chain antibody; antibody; human; BCMA; tumour necrosis factor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated antibody that immunospecifically binds tumor necrosis factor delta, useful for treating, preventing or ameliorating Non-Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                        1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                                   1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                         Length 184;
                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                     100.0%; Score 283; DB 6;
100.0%; Pred. No. 1.2e-25;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP60552 standard; protein; 184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human tumour necrosis factor BCMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-MAY-2002; 2002WO-US016106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                       Local Similarity 100.
108 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-156740/15.
                                                                                                                                                                                                                                               Sequence 184 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP60552;
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                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
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human, disease or disorder such as autoimmune disease, and graft versus host disease (GVHD). The autoimmune disease is systemic lupus erythematosus, rheumatoid arthritis or Sjögren's systemic lupus is useful for detecting, diagnosing, prognosing, treating, preventing or ameliorating a disease or disorder associated with aberrant APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL or APRIL OR APRIL OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIANCE OR APPLIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, TACI, BR3, receptor; tumour necrosis factor ligand; TNF ligand;
TALL-1; April; systemic lupus erythematosus; BCMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding a TACIs or BR3 polypeptide, useful for preparing a composition for treating systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preparing a composition for treating systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLQMAGGCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MLÓMAGÓCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 283; DB 6;
100.0%; Pred. No. 1.2e-25;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of human BCMA receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP97717 standard; protein; 184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 2; 153pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ridgway J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2001; 2001US-0310114P. 30-APR-2002; 2002US-0377171P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUL-2002; 2002WO-US023487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-256560/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2003014294-A2
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The present invention describes an isolated polymucleotide (I), which is overexpressed in haematological malignancies, and which encodes a coverexpressed in haematological malignancies, and which encodes a confront of the polypeptide. Also described: (1) an isolated polypeptide; (2) an expression vector comprising (I) operably linked to an expression control sequence; (3) a comprising an expression vector; (4) an isolated antibody that specifically binds to the polypeptide or its immunogenic fragment; and (5) immunoconjugates comprising the antibody above, or an antibody that specifically binds to a polypeptide, or its immunogenic fragment, encoded by (I). (1) has cytostatic and immunotherapy. The immunoconjugates are useful in the manufacture of a medicament, particularly as active ingredients in a composition for treating cancer, e.g. multiple myeloma call, chronic lowleamia, B cell leukaemia, Der Il leukaemia, B cell leukaemia, Der Il leukaemia, Der Il leukaemia, Der Il leukaemia, Der Il leukaemia, Der Il leukaemia, Der Il leukaemia, Der Il leukaemia, Der Il leukaemia, Cancer, agente, and generating antibodies or immunoconjugates for treating cancer agente, and generating antibodies or immunoconjugates for treating or primetes agente, and generating antibodies or immunoconjugates for treating contractive in the hapmatolonical maliannical adecribed have
                                                                                                                                                                                                                                                                                                                                                               haematological malignancy; immunoconjugate; cytostatic; immunostimulant; vaccine; immunotherapy; cancer; multiple myeloma cell; chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    producating the hadmatological malignancies described above. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New hematological malignancy-related genes and polypeptides, useful for screening anti-cancer agents, and generating antibodies or immunoconjugates for treating e.g. multiple myeloma cell or chronic
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang A, Ordonez N;
                                                          1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                   indels
    Pred. No. 1.2e-25; ; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mannion J, Clapper JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; SEQ ID NO 4; 307pp; English.
                                                                                                                                                                                                    ADD67527 standard; protein; 184 AA.
                                                                                                                                                                                                                                                                                                                            Human Ly1732P protein SEQ ID NO:4.
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0
100.0%;
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                                                                                                                                                                                                                                                                                    (first entry)
                       51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaiger A, Algate PA,
Carter L, Mcneill PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lymphocytic leukemia.
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    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel method for treating a neurodegenerative immunological disorder, demyelination or Central Nervous System (CNS) inflammation in a mammal. The method comprises administering B-cell maturation antigen (BCMA), or an antibody against BCMA or a BCMA igand (the mammal has or is at risk of developing multiple sclerosis). The method of the invention has neuroprotective, nootropic, and antiinflammatory activity, and may have a use in gene therapy. The methods, BCMA, and antibodies are useful for treating a neurodegenerative immunological disorder such as multiple sclerosis, demyelination or CNS inflammation. The present sequence represents human BCMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating a neurodegenerative immunological disorder, e.g. demyelination or inflammation in a mammal comprises administering a B-cell maturation antigen (BCMA), an antibody against BCMA or a BCMA ligand.
                                                                                                                                                                                                                                                                                           human, neurodegenerative immunological disorder; demyelination;
Central Nervous System; CNS; inflammation; B-cell maturation antigen;
BCMA; multiple sclerosis; neuroprotective; nootropic; antinflammatory;
                                Gaps
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                                                                            1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                            1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
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                Pred. No. 1.2e-25;
Mismatches 0;
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                                                                                                                                                                                                                                                              Human B-cell maturation antigen SEQ ID NO:1.
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                                                                                                                                                                      ADG43715 standard; protein; 184 AA
100.08; Pr. 0;
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                                                                                                                                                                                                                                  (first entry)
                             51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BIOJ ) BIOGEN INC
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                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                              gene therapy
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                                                                                                                                                                                                   ADG43715;
             Best Local
Matches 5
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                                                                                                                                     RESULT 15
ADG43715
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Search completed: February 26, 2005, 20:45:21 Job time : 54.0383 secs

100.0%; Score 283; DB 7; Length 184;

Query Match

Sequence 6, Appli Sequence 5, Appli Sequence 9, Appli Sequence 3, Appli Sequence 3, Appli Sequence 11, Appli Sequence 7, Appli Sequence 7, Appli Sequence 13, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 147, Appli Sequence 15, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 75, Appli Sequence 75, Appli Sequence 75, Appli Sequence 76, Appli Sequence 76, Appli Sequence 76, Appli Sequence 77, Appli Sequence 76, Appli Sequence 77, Appli Sequence 77, Appli Sequence 77, Appli Sequence 77, Appli Sequence 77, Appli Sequence 77, Appli

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Length 184;
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US-10-028-248A-75
US-10-107-782-75
US-09-855-158-6

US-09-854-864-5

US-09-855-188-9

US-09-855-158-9

US-09-855-158-3

US-10-077-438-3

US-10-077-438-3

US-10-077-438-3

US-10-077-438-3

US-10-077-438-3

US-10-077-438-3

US-09-855-158-7

US-09-855-158-7

US-09-855-158-13

US-09-855-158-11

US-09-855-158-11

US-09-855-158-11

US-09-855-158-11

US-09-855-158-11

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US-10-107-782-74
US-10-152-363A-62
US-09-779-050A-45
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Publication No US20020165156A1
GENERAL INFORMATION:
APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Tachopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Immunorequiatory Agent
FILE OF INVENTION: Immunorequiatory Agent
FILE OF INVENTION: Immunorequiatory Agent
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FILE OF INVENTION: Immunorequiatory Agent
FILE OF INVENTION INVERSE: 60/149,378
FRIOR FILING DATE: 1999-08-17
FRIOR FILING DATE: 2000-02-18
FRIOR FILING DATE: 2000-02-18
FRIOR FILING DATE: 2000-02-18
FRIOR FILING DATE: 2000-02-18
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US-09-855-158-12
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US-09-855-158-20
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SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 184
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181
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     TYPE: PRT
     Sequence 1, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 7, Appli
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Sequence 17, Appli
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                                                                                                                                                                     February 26, 2005, 20:41:13; Search time 38.6298 Seconds (without alignments) 433.092 Million cell updates/sec
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                                                                                                                                                                                                                                                                US-10-077-438-1_COPY_1_51
283
1 ML@MAGQCSQNEYFDSLLHA.....TPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published Applications AA:*

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                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-077-438-7
US-10-077-137-1
US-10-068-725-2
US-10-115-1882-47
US-10-1088-63-7
US-10-115-192-8
US-10-115-192-8
US-10-108-063-7
US-10-108-063-7
US-10-115-192-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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Sequence 45, A Sequence 20, A Sequence 20, A Sequence 15, A

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US-09-854-864-6

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1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKG 51
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Sequence 2, Application US/10068725

Sequence 2, Application US/10068725

Publication No. US20030012783A1

GENERAL INPORMATION:
TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
FILE REPRENCE: 01-04

CURRENT APPLICATION NUMBER: US/10/068,725

CURRENT FILING DATE: 2002-02-06

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-04-22

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 184
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                                                                                                                            Query Match 100.0%; Score 283; DB 13; Best Local Similarity 100.0%; Pred. No. 1.7e-25; Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ALGORIAN DELLICY
APPLICANT: ABOTECH RED S.A.
TITLE OF INVENTION: BEEF Receptor (BCMA), An
TITLE OF INVENTION: Immunoregulatory Agent
FILE REFERENCE: A080PCT Immunoregulatory Agent
FILE REFERENCE: A080PCT SOULOS-15
PRIOR PRILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-18
NUMBER: OF SEQ ID NOS: 8
SOFTWARE: FRASESO for Windows Version 4.0
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Publication No. US20020172674A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MacKay, Fabienne
APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Tschopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT; ORGANISM: homo sapien
US-10-077-137-7
                      TYPE: PRT
ORGANISM: homo sapien
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LENGTH: 184
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 283; DB 13; Best Local Similarity 100.0%; Pred. No. 1.7e-25; Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                          APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Techopp, Jurg
APPLICANT: Techopp, Jurg
APPLICANT: Thompson, Jeffrey
APPLICANT: Thompson, Jeffrey
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
TITLE OF INVENTION: Immunoregulatory Agent
FILER REPERENCE: A080PCT
CURRENT APPLICATION NUMBER: US/10/077,438
CURRENT PILING DATE: 1999-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immunoregulatory Agent
FILE REFERENCE: A080PCT
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PRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 1999-08-17
PRIOR PLING DATE: 2000-02-11
PRIOR PLING DATE: 2000-02-11
PRIOR PLING DATE: 2000-02-18
PRIOR RILING DATE: 2000-02-18
PRIOR RILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/181,684
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536
PRIOR FILING DATE: 2000-02-18
                                                                                                                                                                                 Sequence 7, Application US/10077438 Publication No. US20020165156Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10077137
Publication No. US20020172674A1
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Ambrose, Christine
Tschopp, Jurg
Schneider, Pascal
Thompson, Jeffrey
                                                                                                                                                                                                                                                                      APPLICANT: MacKay, Fabienne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: homo sapien
US-10-077-438-7
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LENGTH: 184
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Gaps

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Sequence 11, Application US/10216074
Publication No. US20030148445A1
GENERAL INFORMATION:
APPLICANT: Shu, Hong-Bing
ITILE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
ITILE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 2879-72
CURRENT APPLICATION NUMBER: US/10/216,074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
             1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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APPLICANT: Gross, Jane A.
APPLICANT: Henne, Randal M.
APPLICANT: Henne, Randal M.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor FILE REFERENCE: 00-103
CURRENT APPLICATION NUMBER: US/10/008,063
CURRENT PILION DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-152-363A-27
US-10-152-363A
| Sequence 27, Application US/10152363A
| Publication No. US20030103986A1
| GENERAL INFORMATION:
| APPLICANT: Rixon, Mark W.
| APPLICANT: Gross, Jane A.
| TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins Prins REPERBURE: 01-20
| FILE REPERBURE: 201-20
| CURRENT FILING DATE: 2002-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 283; DB 14; Best Local Similarity 100.0%; Pred. No. 1.7e-25; Matches 51; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 100.0%; Score 283; DB 14; 1 Similarity 100.0%; Pred. No. 1.7e-25; 51; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 27
LENGTH: 184
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PRIOR APPLICATION NUMBER: 60/293,343
PRIOR FILING DATE: 2001-05-24
                                                                                                                                  Sequence 7, Application US/10008063; Publication No. US20030092164A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-10-008-063-7
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TYPE: PRT
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Publication Nd. US20030059862A1
GENERAL INFORMATION:
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REPERENCE: PFS54
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRICR FILING DATE: 2001-05-24
NUMBER OF SEG ID NOS: 48
SOFTWARE: PatentIn version 3.0
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                                                                                                           Length 184;
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APPLICANT: Biogen, Inc.
TILE OF INVENTION: April Receptor (BCMA) and Uses Thereof
FILE REFERENCE: Agaid Receptor (BCMA) and Uses Thereof
FILE REPERENCE: April Receptor (BCMA) and Uses Thereof
FILE REPERENCE: 2002-04-02
FRIOR PRILING DATE: 2000-04-02
FRIOR FILING DATE: 2000-06-30
FRIOR FILING DATE: 2000-02-11
FRIOR FILING DATE: 2000-02-11
FRIOR FILING DATE: 1000-02-11
FRIOR FILING DATE: 1000-02-11
FRIOR FILING DATE: 1000-02-11
FRIOR FILING DATE: 1000-10-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                            Indels
                                                                                                     Query Match | 100.0%; Score 283; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 51; Conservative 0; Mismatches 0;
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100.0%; Score 283; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.7e-25;
Matches 51; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match | 100.0
Best Local Similarity 100.0
Matches 51, Conservative
; TYPE: PRT ; ORGANISM: Homo sapiens US-10-068-725-2:
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ORGANISM: Hdmo sapiens
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US-10-115-192-8
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WS-09-854-864-6

i Sequence 6, Application US/09854864

j Sequence 6, Application US/09854864

j Sequence 6, Application US/09854864

j Setent No. US-0020001296A1

j SENIERAL INFORMATION:

j APPLICANT: THEILL, LARS EXDE

j TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

j TITLE OF INVENTION: BLYS/AGP-3, AND TACI

j TITLE OF INVENTION: BLYS/AGP-3, AND TACI

j TITLE OF INVENTION: WIMBER: US/09/854,864

CURRENT PILING DATE: 2001-09-11

p RIOR FILING DATE: 2000-05-12

p RIOR FILING DATE: 2000-05-12

p RIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

j SOFTWARE: PATENTIA VERSION 3.1

j SOFTWARE: PATENTIA VERSION 3.1
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Publication No. US20020086018A1
Publication No. US20020086018A1
AEPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
TITLE OF INVENTION: 3, AND TACI
FILE REPERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
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Pred. No. 2.8e-25;
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Pred. No. 2.1e-24;
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               CURRENT APPLICATION NUMBER: US/10/115,192
CURRENT FILING DATE: 2002-04-02
PRIOR PRILID DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/181807
PRIOR APPLICATION NUMBER: 60/181807
PRIOR APPLICATION NUMBER: 60/157933
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ FOR WINDOWS Version 4.0
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Best Local Similarity 100.0%; Pr
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ORGANISM: homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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APPLICANT: Markwaitz, Sanford David H.
APPLICANT: Markwaitz, Sanford David H.
APPLICANT: Markwaitz, Sanford David
APPLICANT: Bos Bactechnology, Inc.
APPLICANT: Case Western Reserve University
TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for
TITLE OF INVENTION: Modulators of Metastatic Colorect
TITLE OF INVENTION: Modulators of Metastatic Colorect
TITLE OF INVENTION: Modulators of Metastatic Colorect
TITLE OF INVENTION: MODULES: 2002-10-25
FILE REFERENCE: 018501-00840US
CURRENT FILING DATE: 2001-02-27
FRIOR PILING DATE: 2001-04-02
PRIOR FILING DATE: 2001-04-02
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: US 60/281,149
PRIOR FILING DATE: 2001-04-07
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 283; DB 14; 100.0%; Pred. No. 1.7e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
               PRIOR APPLICATION NUMBER: US/09/565,423
PRIOR FILING DATE: 2000-05-05
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-01
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 11
LENGTH: 184
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2003-03-12
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LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT FILING DATE:
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US-10-087-080-39
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Sequence 5, Application US/09854864

Patent No. US20020081296A1

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: YU, GANG

TITLE OF INVENTION:

FILE REFERENCE: A-666B

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-05-12

PRIOR PILING DATE: 2000-05-12

PRIOR PILING DATE: 2000-05-12

PRIOR PILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 5: 31

LENGTH 181

LENGTH 181
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                                                                                                                                                                                                                               Query Match 95.1%; Score 269; DB 9; Length 51; Best Local Similarity 100.0%; Pred. No. 2.1e-24; Matches 48; Conservative 0; Mismatches 0; Indels
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; PRIOR APPLICATION NUMBER: US 60/204,039; PRIOR FILING DATE: 2000-05-12; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1; SEQ ID NO 6; LENGTH: 51; TYPE: PRT
; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

February 26, 2005, 20:37:33; Search time 49.0468 Seconds (without alignments) 532.472 Million cell updates/sec Run on:

US-10-077-438-1_COPY_1_51
283
1 MLQWAGQCSQNBYFDSLLHA.....TPPLTCQRYCNASVTNSVKG 51 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
; Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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* Query Match	100.0	100.0	64.0	25.8	25.6	25.6	25.6	25.3	25.1	24.9	24.7	24.6	24.6	24.2	24.2	23.9	23.7	23.1	23.0	22.8	22.8	22.8	22.8	22.6	22.4	22.4	22.4	22.3	22.3	22.3
Score	283	283	181	73	72.5	72.5	72.5	71.5	71	70.5	70	69.5	69.5	68.5	68.5	67.5	67	65.5	65	64.5	64.5	64.5	64.5	64	63.5	63.5	63.5	63	63	63
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Q8cfa7 mus musculu Q9d351 mus musculu Q8d351 mus musculu Q81266 homo sapien Q72548 homo sapien Q17969 caenorhabdi Q989310 g sortilin-Q6bg85 paramecium P46687 arabidopsis Q8vx81 drosophila Q22423 caenorhabdi Q9vx91 drosophila Q2423 caenorhabdi Q9vtr9 drosophila Q7z6f5 homo sapien
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The Europeah Bioinformatics Institute. There are no restrictions on its web yn ono-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-!- DISEASE: Involved in a form of T-cell acute lymphoblastic leukemia (T-ALL) by a chromosomal translocation t(4,16) (q26,p13) which involves TNFRSF17 and IL2.
-!- SIMILARITY: Contains 1 TNFR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTIONS WITH TRAFS AND TRAF6.

MEDILMES20381333; PubMed=10908663; DOI=10.1073/pnas.160213497;
Shu H.-B., Johnson H.;
"B cell maturation protein is a receptor for the tumor necrosis factor
                                                                                                        Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C., Inoue J.-I., Devergne O., Tsapis A.; Thoue J.-I., Devergne O., Tsapis A.; The receptor family member BCMA (B cell maturation) associates with TNF receptor associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-I, c-Jun N-terminal kinase, and p38 mitogenactivated protein kinase.";
"NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu)."; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                             MEDLINE-20259066, PubMed=10801128, DOI=10.1038/35010115,
Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
Madden K., Ku W., Partish-Novak J., Foster D., Lofton-Day C.,
Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
Harrison K., Kindsvogel W., Clegg C.H.;
"TACI and BCMA are receptors for a TNF homologue implicated in B-cell
autoimmune disease.";
Nature 404:995-999(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.
MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
"APRIL and TALL-I and receptors BCMA and TACI: system for regulating humoral immunity.";
                                                                           FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0016021; C:integral to membrane; TAS. GO:0005886; C:plasma membrane; TAS. GO:0004872; F:receptor activity; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S43486; S43486.
PDB; 10QD; X-ray; K/L/M/N/O/P/Q/R=8-46.
Genew; HGNC:11913; TNFRSF17.
                                                                                           MEDLINE=20363816; PubMed=10903733;
                                                                                                                                                                                                                           J. Immunol. 165:1322-1330(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nat. Immunol. 1:252-256(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AB052772; BAB60895.1; -. AY509112; AAR84240.1; -.
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ESCUENCE FROW N.A.

TISSUE-Pooled,

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X. TISSUE-Pooled,

RELINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ralausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buerock K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Detchenko, L., Marusina M.F., Farmer A.A., Rubin G.M., Hong L.,

B Capleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachey J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rachiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0007275; P:development; TAS.
GO; GO:0007165; P:signal transduction; TAS.
3D-structure; Chromosomal translocation; Immune response;
Bolymorphism; Proto-oncogene; Receptor; Signal-anchor; Transmembrane.
DOMAIN
1 54 Extracellular (Potential).
TRANSMEM 55 77 Signal-anchor for type III membrane
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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277AF11E2767D932 CRC64;
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05-UTL-2004 (TrEMBLrel. 27, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Tumor necrosis factor receptor superfamily, member 17.
                                                                                                                                                                                                                                Cytoplasmic (Potential)
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Best Local Similarity
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   RC STRAIN-C57BL/64; TISSUB-COLON;

RE SCROBENCE FROW N.A. (120/US-COLON;

RA OAGAZAKI Y., FURUNO M., KASUKAWA T., Adachi J., BOND H., KONGO S.,

RA OKAZAKI Y., FURUNO M., KASUKAWA T., Adachi J., BOND H., KONGO S.,

RA NIKAIGO I., OGATO N., SAILORR., SUZUKI H., YAMMANAR I., KIVOSAWA H.,

RA AGIA K., TOMATU Y., HASEGGAWA T., NOGAMI A., SCHONDACH C., GOJODORI T.,

RA AGAILA E., Bradt D., BULUE C., HUME D.A., QUACKENDUSH J.,

RA GASTERLAND T., GATIBOLDI M., GISSI C., GOZGIK A., FRAZER K.S.,

RA GASTERLAND T., GATIBOLDI M., GISSI C., GOZGIK A., FRAZER K.S.,

RA GASTERLAND T., GATIBOLDI M., GISSI C., GOZGIK A., RA, GOUGH J.,

RA KANAJI H., KAWASAW Y., KEGZIERSKI R.M., KING B.L.,

KONAGAYA A., KURCCHKIN I.V., LEV Y., LENHARD B. D.,

RA MAGASIMMA T., NUMMARA K., OKIGO T., PRVAN W.J., PERTEG G., PESOLE G.,

RA PELYOVSKY N., PILLAIS L., MARCHIONNI L., MKENZIEL L., MIKI H.,

RA NGGABAIMA T., NUMMARA K., OKIGO T., PRVAN W.J., PERTEG G., PESOLE G.,

RA SANGELIN A., Schneider C., Semple C.A., Secou M., Shimada K.,

SANGELIN A., Schneider C., Semple C.A., Secou M., Shimada K.,

SANGELIN A., Schneider C., Semple C.A., Secou M., Shimada S.,

MILMING L.G., WyNENAW-BORIS A., YANAGISHAW M., YANG I., YANG I.,

RA YUAN Z., ZAVOLAN M., ZIM Y., ZIMMER A., YANGISHAW M., YANG I., YANG I.,

RA YUAN Z., ZAVOLAN M., ZANU Y., ZIMMER A., YARAWAW T., PKARWAW T., PKARWAW T.,

RA HYROZANG-KIBHKAWA T., KONDO H., NAKAMURA M., SARAZUME N.,

RA HATRA A., HASHIZUME W., IMOLANI K., ISHIBI K., ISHIBAGAW K., ARAKWAW T., PKARWAW I.,

RA HATRA A., HASHIZUME W., IMOLANI K., ISHIBAGAW R., SHINAGAWA I.,

RA HATRA A., HASHIZUME W., IMOLANI K., ISHIBAGAW R., SHINAGAWA I.,

RA HATRA A., HASHIZUME W., IMOLANI K., ISHIBAGAW R., SHINAGAWA I.,

RA HATRA A., HASHIZUME W., IMOLANI K., ISHIBAGAWA R., SHINAGAWA I.,

RA HATRA A., HASHIZUME W., IMOLANI Y., SHINAGAWA I.,

RA HATRA A., HASHIZUME W., IMOLANI Y., SHINAGAWA I.,

RA YABUNISHI A., SAKAI K., SASAKI D., SHINAGAWA I.,

RA YABUNISHI A., SAKAI K., SASAKI D., SHINAGAWA I.,

RA YABUNISHI A., SAKAI W., SAKAI W.,

RA Y
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                                                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
STRAIN=BALB/C; TISSUE=Spleen;
MEDLINE=9906115; Pubmed=984669;
Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A.,
Le Coniat M., Mornon J.P., Berger R., Tsapis A.;
"The characterization of murine BCMA gene defines it as a new if the tumor necrosis factor receptor superfamily.";
                                                                                                                                                                                                                                                                                    MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 17 (B-cell
                                                                                                                                                                                                100.0%; Score 283; DB 2; Length 184;
                                                                                                                                                                                                Score 200,
Pred. No. 4e-27;
                                                                           Strausherg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC058291; AAHS8291.1; -.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                 184 AA; 20139 MW; C7ACF9B40FC5531A CRC64;
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                   185 AA.
                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  maturation protein).
Name=Tnfrsf17; Synonyms=BCM, BCMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                 100.08;
                                                                                                                                                                                                                Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                 TR17 MOUSE
088472;
                                                                                                                                                  Receptor.
                                                                                                                                                               SEQUENCE
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Matches
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SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN=C5288625; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetcow K.H., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhar N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Heith F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Rachards S., Worley K.C., McEwran K.J., Malek J.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hold S., Shorchenko Y., Boulfard G.G.,

Mhiting M., Madan A., Young A.C., Schwutz J., Myers R.M.,

Blakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodisjuez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Robertation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse CDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-!- FUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.

Promotes B-cell survival and plays a role in the regulation of humoral immunity. Activates NP-kappa-B and JNK (By similarity).

-!- SUBUNIT: Associates with TRAFI, TRAF2, TRAF3, TRAF5 and TRAF6 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thymus, bone marrow and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extracellular (Potential).
Signal-anchor for type III membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SUBCELLULAR LOCATION: Type III membrane protein (Probable).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1343050; Tnfrsf17.
Alternative splicing; Immune response; Receptor; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 181; DB 1; Length 185; Pred. No. 1.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8806352B4FD26A8E CRC64;
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By similarity.
By similarity.
Missing (in isoform 2).
/FTIG-VSP_006507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein (Potential).
Cytoplasmic (Potential).
TNFR-Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- TISSUE SPECIFICITY: Detected in spleen, thymus, heart, and at lower levels in kidney and lung.
-1- SIMILARITY: Contains 1 TNFR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :soId=088472-2; Sequence=VSP_006507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=088472-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF061505; AAC23799.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK020247; BAB32038.1; -. EMBL; BC027519; AAH27519.1; -. HSSP; Q02223; 10QD.
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36
18
32
36
91
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70
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
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Gaps

7;

Length 499;

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STRAIN=C57BL/6J;
MEDLINE=22563400; PubMed=12676567; DOI=10.1016/S0888-7543(03)00036-3;
Desseyn J.-L., Laine A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1674 AA; 181168 MW; 3BC42CB004476309 CRC64;
                                                   499 AA; 54190 MW; 04F89EF4F23EE61E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escande F., Buisine M.P.;
"The mouse secreted gel-forming mucin gene cluster.";
Biochim. Biophys. Acta 1676:240-250(2004).
EMBL; AJS11867; CADS4415.1; -..
EMBL; AJS11868; CADS4415.1; JOINED.
HSSP; O46162; 1KJ0.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=14984930; DOI=10.1016/j.bbaexp.2004.01.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 72.5; DB 2;
Pred. No. 4.6;
1; Mismatches 7;
                                                                                                      DB 2;
                                                                                                    Score 72.5; DI
Pred. No. 1.3;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1181 ČŠÓNĖYFDHSEGTČVPČ-----APPTT 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 2850 AA
                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1674 AA
                                                                                                                                                                                                                                        8 CSQNEYFDSLLHACIPCQLRCSSNTPPLT 36
                                                                                                                                                                                                           8 CSONEYFDSLLHACIPCOLRCSSNTPPLT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secreted gel-forming mucin (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:2663233; Muc6.
InterPro; IPR002919; Cysrich TIL.
InterPro; IPR00941; PMP_SGCI.
InterPro; IPR001846; VWF_D.
                                                                                                      25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 25.6%;
Best Local Similarity 48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 24, (TrEMBLrel. 24, (TremBLrel. 26,
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Pfam; PF00094; VWD; 3.
SMART; SM00216; VWD; 3.
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          Gaps
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Mus musculus (Moulse).
Eukaryota hetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
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                                                           4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG 51
                                                                                         1 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 25.8%; Score 73; DB 2; Length 718; Local Similarity 26.5%; Pred. No. 1.7; Losservative 7; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 QMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKG
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BEDLINE-21428166; PubMed=11545438;
Willhoeft U., Campos-Gongora B., Touzni S., Bruchhaus I.,
"Introns of Entamoeba histolytica and Entamoeba dispar.";
     8; Indels
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ010752; CAA09343.1;
HSSP; A5682; HCV.
HSSP; MGJ:26682; HCV.
InterPro; IPR002919; Cysrich_IIL.
InterPro; IPR001846; WWF_D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              718 AA; 80231 MW; FFF6362A49F2827A CRC64;
                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
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          4; Mismatches
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EMBL, AJ409106, CAC34072.1; -.

InterPro; IPR006212; Furin repeat.

InterPro; IPR0909030, Grow_Fac_recept.

SMART; SM00261; FU; 6.
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01-NOV-1998 (TrEMBLrel. 08, Last sequ
01-NAR-2004 (TrEMBLrel. 26, Last anno
Gastric mucin-like protein (Fragment)
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Eukaryota; Entamoebidae; Entamoeba.
NCB1_TaxID=5759;
          34; Conservative
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Pfam; PF00094; VWD; 1.
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SMART; SM00216; VWD; 1.
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MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

MACAZAKI Y. FUTUND M., KASUKAWA T., Adachi J., Bono H., Kondo S.,

Mikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

Madarelli R., Hilli D.P., Bult C., Hume D.A., Quackenbush J.,

Baldarelli R., Hilli D.P., Bult C., Hume D.A., Quackenbush J.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Blake J.A., Bradt D., Hetcher C.F., Forrest A., Frazer K.S.,

Malla E., Dragani T.A., Fletcher C.F., Forrest A., Gudph J.,

Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,

Konagaya A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Maglott D.R., Pontius J.U., Qi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,

Milming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21177254; PubMed=10881172; DOI=10.1038/76889;
Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
"Identification of a receptor for BLyS demonstrates a crucial role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     095135; 090B23; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) 05-JUL-2004 (Rel. 44, Last annotation update) acrossis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).
   conservation of the
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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PROSITE; P901225; CTCK 2; 1.
SEQUENCE 2850 AA; 300398 WW; 9CD95F0845C79C9D CRC64;
"Characterization of mouse muc6 and evidence of conserva gel-forming mucin gene cluster between human and mouse." Genomics 81:433-436 (2003).
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                                                                                               PRT;
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InterPro; IPR00207; Cys Knot C.
InterPro; IPR009041; PMP_SGGI.
InterPro; IPR001046; VWF_D.
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Pfam; PF00094; VWD; 3
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MGD; MGI:2663233; M
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Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazuwa N., Sato K., Hirozane N., Sato K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; Birney E., Lander E.S., Rogers J., Enney E., Hayashizaki Y.; All Marchione Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous Linghous
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MEDLINE=20341628; Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,
Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,
Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,
Meng S.-Y., Boyle W.J., Hgu H.;
"TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis
factor family member involved in B cell regulation.";
J. Exp. Med. 192:137-143(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITE=21322748; PubMed=11429548; DOI=10.1038/89782;
Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
"TACI-ligand interactions are required for T cell activation and
collagen-induced arthritis in mice.";
Nat. Immunol. 2:632-637(2001).
Immunol. 2:632-637(2001).
Ithat binds both ligands with similar high affinity. Mediates
calcineurin-dependent activation of NP-AT, as well as activation
of NP-Kappa-B and AP-I. Involved in the stimulation of B- and T-
cell function and the regulation of humoral immunity (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal domain of CAMLG with its C-terminus (By similarity).
-!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
-!- SIMILARITY: Contains 2 TNFR-Cys repeats.
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GO; GO:0005887; C:integral to plasma membrane; IDA.

GO; GO:0005031; F:tumor necrosis factor receptor activity; IDA.

InterPro; IPR001368; TRFR C6.

PROSITE; PS00652; TNFR NGFR 1; FALSE NEG.

PROSITE; PS50050; TNFR NGFR 2; FALSE NEG.

Immune response; Receptor; Repeat; Signal-anchor; Transmembrane.

DOMAIN 129 149 Signal-anchor for type III membrane

Signal-anchor for type III membrane
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I > P (in Ref. 2).
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Cytoplasmic (Potential)
TNFR-Cys 1.
TNFR-Cys 2.
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Pred. No. 0.86;

Best Local Similarity

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NCBI_TaxID=10090;
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01-FBB-1995 (Rel. 31, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Proprotein convertase subtlishin/kexin type 5 precursor (BC 3.4.21.-)
(Proprotein convertase PC5) (Subtlishin/kexin-like protease PC5) (Subtlishin-like proprotein convertase PC5) (Subtlishin-like proprotein convertase PC5)
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PubMed=15296759; D01=10.1016/j.cub.2004.07.029;
PubMed=15296759; D01=10.1016/j.cub.2004.07.029;
Gromadka M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,
Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,
Cohen J., Meyer E., Sperling L.;
Chiph Coding Density on the Largest Paramecium tetraurelia Somatic
Chromosome."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
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protein with EGF domains and furin-like repeats.
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
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"Paramecium, megabase sequencing project.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343821 MW; D8CC6A247876A5A5 CRC64;
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InterPro; IPRO060545; CytC heme BS.
InterPro; IPRO060345; CytC heme BS.
InterPro; IPRO06212; Furin repeat.
InterPro; IPRO06212; Furin repeat.
InterPro; IPRO06210; IEGF.
InterPro; IPRO0610; IEGF.
SWART; SWOO181; EGF. 22.
R SWART; SWOO181; EGF. 22.
R PROSITE; PS00197; 2FE2S FERREDOXIN; UNKNOWN 1.
PROSITE; PS00199; CYTOCHEONE.C; UNKNOWN 2.
PROSITE; PS0196; EGF. 2; 12.
R SEQUENCE 3005 AA; 343821 MW; DRCCFADATORERY
    13;
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                                      CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 41
                                                               | :::|:|:| :|:| :| :| :| :| CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38
                                                                                                                                                                                 PRT; 3005 AA.
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8; Mismatches
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  Mismatches
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Conservative
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                                                                                                                                                                                                                                                                                                                             Paramecium tetraurelia.
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12;
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DEVELORMENTE ACTERISTION.

MEDIINE=97436919; PubMed=2291583;

DOI=10.1002/(SICI)1520-6408(1997)21:1<75::AID-DVG9>3.3.CO;2-T;

BARGOURT S.L., RARGOURT D.R.;

"Murine subtilisin-like proteinase SPC6 is expressed during embryonic implantation, somitogenesis, and skeletal formation.";

Dev. Genet. 21:75-81(1997).

-I-FUNCTION: Likely to represent a widespread endoprotease activity within the constitutive and regulated secretory pathway. Capable of cleavage at the RX(K/R)R consensus motif. May be responsible for the maturation of gastrointestinal peptides. May be involved in the cellular proliferation of adrenal cortex via the activation of growth factors.

-I-CATALITIE ACTIVITY: Release of mature proteins from their activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proproteins by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa Can be any amino acid and Yaa is Arg or Lys.
SUBCELLULAR LOCATION: PCSA is secreted through the regulated secretory pathway. PCSB is a type I membrane protein localized to a paranuclear post-Golgi network compartment in communication with
                                                                            MEDLINE=93327934; PubMed=8335106; DOI=10.1016/0014-5793(93)80163-O; Nakagawa T., Murakami K., Nakayama K.; "Identification of an isoform with an extremely large Cys-rich region of PC6, a Kex2-like processing endoprotease."; FEBS Lett. 327:165-171(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isoid=Q04592-1; Sequence=Displayed;
Name=PC5A; Synonyms=Short;
Isoid=Q04592-2; Sequence=D05438, VSP_005439;
TISSUB SPECIFICITY: PC5A is expressed in most tissues but is most abundant in the intestine and adrenals. PC5B is expressed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96293359; PubMed=8698813; DOI=10.1083/jcb.134.1.181; Constam D.B., Calfon M., Robertson E.J.; SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone morphogenetic proteins at distinct sites during embryogenesis."; J. Cell Biol. 134:181-191(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Adrenal cortex;
MEDLINE=93342056; PubMed=8341687;
Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
"CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a candidate proprotein convertase expressed in endocrine and nonendocrine cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97103178; PubMed=8947550; DOI=10.1083/jcb.135.5.1261; Be Bie I., Marchinktewicz M., Malide D., Lazure C., Nakayama K., Bendayan M., Seidah N.G. **

"The isoforms of proprotein convertase PC5 are sorted to different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification and functional expression of a new member of the mammalian Kex2-like processing endoprotease family: its striking structural similarity to PACE4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 90:6691-6695(1993)
SEQUENCE OF 330-1877 FROM N.A. (ISOFORM PC5B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL SEQUENCE, AND SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM PCSA). TISSUE=Brain, and Intestine; MEDLINE=93224489; PubMed=8468318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subcellular compartments.";
J. Cell Biol. 135:1261-1275(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM PCSA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. 113:132-135(1993).
                                               STRAIN=ICR; TISSUE=Intestine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=PC5B; Synonyms=Long;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          early endosomes.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL EXPRESSION
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intestine, adrenals and lung but not in the brain.

-I-BOYELOPMENTAL STAGE: Weakly expressed throughout the embryo, except in the developing nervous system, the ribs and the liver, but markedly up-regulated at discrete sites during development. At ES.5, prominent expression observed in differenciated decidua. At ES.5, prominent expression in extreambyronic endoderm, amnion and nascent mesoderm. At ES.5, abundant expression in somites and yolk sac followed by a confination to dermamyotome compartment. Between ES.5 and ES.1.5, abundant expression in AER (thickened ectodermal cells of limb buds). At ES.5, expression in the limbs is confined to the condensing mesenchym surrounding the cartilage. At this stage, strong expression also detected in vertebral and facial cartilage primordia and in the muscle of the tongue. At ES.5, abundant expression in epithelial cells of the intestinal villi leoform A is most abundant at all stages but significant levels of isoform B occur at ES.5.

-I- DOWAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between this Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      -!- DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain sorting information. AC 1 directs TGN localization and interacts with the TGN sorting protring PACS-1.
-!- SIMILARITY: Belongs to the peptidase S8 family.
-!- SIMILARITY: Contains 1 homo B/P domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proprotein convertase subtilisin/kexin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cleavage (auto-) (By similarity).
Cell attachment site (Potential).
Charge relay system (By similarity)
Charge relay system (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternative splicing, Cleavage on pair of basic residues,
Direct protein sequencing, Glycoprotein, Hydrolase, Repeat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cys-rich motif (CRM) region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct protein sequencing; Glycoprotein; Hydrol:
Serine protease; Signal; Transmembrane; Zymogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:97515; Pcak5.
InterPro; IPR006211; Furin-like.
InterPro; IPR009030; Grow_fac_recept.
InterPro; IPR009030; Grow_fac_recept.
InterPro; IPR009020; Pcpt_inh_propept.
InterPro; IPR00284; PrproinconvertsP.
Pfam; PF00173; Furin-like; 2.
Pfam; PF00082; Poptidase_S8; 1.
Pfam; PF00082; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILIASIN.
PROSITE; PS00136; SUBTILIASE_ASP; 1.
PROSITE; PS00136; SUBTILIASE_ASP; 1.
PROSITE; PS00136; SUBTILIASE_ASP; 1.
PROSITE; PS00136; SUBTILIASE_ASP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Catalytic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00138; SUBTILASE SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D17583; BAA04507.1; -. EMBL; D12619; BAA02143.1; -. EMBL; L14932; AAA74636.1; -. PIR; A48225; A48225; PIR; S34583; S34583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602
1753
1844
1877
117
523
173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S08.076;
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TRANSMEM
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 MAGQCSQNEYFDSLLHACIPCQLRCSS-------NTPPLTCQRYCNASV 45
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                                                                                                                                                                                                                                                              Gaps
                                                                                                                                        N-linked (GlcNAc. .) (Potential).
GEYIDDQGHCQTCEASCAKCWGPTQEDCISCPVTRVLD
ATEESWAEGGFCMLVKKNNLCQRKVLQQLCCKTCTFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olsen G.J., Sogin M.L.;

"Draft equence of the Giardia lamblia genome.";

"Draft equence of the Giardia lamblia genome.";

Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an

EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is

preliminary data. AACB01000001; EAM13000.1; -.

EMBL; AACB010000001; EAM3000.1; -.

REMEL; AACB010000001; EAM35; CYCC. Heme. BS.

InterPro; IPR000345; CYCC. Heme. BS.

InterPro; IPR002049; Laminin EGF.

REMOSTIE; PS00190; CYTOCHROWE. C; UNKNOWN 2.

RROSTIE; PS01248; LAMINI TYPE EGF; UNKNOWN 1.
           (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
                                                                                                                                                                                                                                                                                               (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=WB C6;
Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Indels 20;
                                                                                                         (Potential)
                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                        Length 1877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 1025;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
NCBI _TaxID=184922;
                                                                                                                                                                                                                                                                                  7 QCSQNEYFDSLLHACIPCQLRCSSNTPP----LTCQRYCNASVTNSVK
                                                                                                                                                                                                        /FTId=VSP_005439.
MW; EC850E2DF20EA1C3 CRC64;
                                                                                                                                                                                             (In isoform PC5A).
  <u>6</u>
                                                                                                         (GlcNAc. . .)
                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
   system
                                                                                                                                                                                                                                         DB 1;
           (GlcNAc...
(GlcNAc...
(GlcNAc...
(GlcNAc...
(GlcNAc...
(GlcNAc...
(GlcNAc...
                                                                                                                               (GlcNAc.
                                                                                                                                                                          (in isoform PC5A)
                                                                                              (GlcNAc
                                                                                                                                                                                     005438
                                                                                                                                                                                                                                                  9.2;
                                                                                                                                                                                                                                                                                                                                                             PRT; 1025 AA
                                                                                                                                                                                                                                        Score 70.5; D
Pred. No. 9.2;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 5.7;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 70;
                                                               N-linked
N-linked
                                                                                                                     N-linked
N-linked
                                                                                                                                                                                   FTIG=VSP
                                                                                     N-linked
                                                                                              N-linked
                                                                                                           N-linked
                                                      N-linked
                                                                                                                                                                                               Missing
                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.7%;
Local Similarity 24.2%;
hes 15; Conservative 8
                                                                                                                                                                                                                                      24.9%;
Local Similarity 34.7%;
les 17; Conservative
                                                                                                                                                                                                                  1877 AA; 209287
                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                GLP 170 141434 144511.
Giardia lamblia ATCC 50803.
                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
388
227
383
383
667
754
804
854
951
1016
1220
1317
1733
915
                                                                                                                                                                                              1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
 388
227
383
667
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1733
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ACT SITE
CARBOHYD
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VARSPLIC
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                                                                                                                                                                                                                                      Query Match
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                                                                                              CARBOHYD
                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                            Q7R6J7
Q7R6J7;
                                                                                                                                                                                                                                                             Matches
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ZAN MOUSE STANDARD; PRT; 5376 AA. 088799; 008647; 16-007-2001 (Rel. 40, Last sequence update) 25-007-2004 (Rel. 45, Last annotation update)
                                                                                                                                                                                                                                   MEDLINE=21138439; PubMed=11239002; DOI=10.1093/nar/29.6.1352; Wilson M.D., Riemer C., Martindale D.W., Schnupf P., Boright A.P., Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C., Miller W., Koop B.F.; Chemperative analysis of the gene-dense ACHE/TRRZ region on human chromosome 7q22 with the orthologous region on mouse chromosome 5."; Nucleic Acids Res. 29:1352-1365(2001).
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.6%; Score 69.5; DB 2; Length 5374; 36.8%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GG; GG:0016020; C:membrane; IEA.
GG; GG:0007339; P:binding of sperm to zona pellucida; IEA.
GG; GG:0007155; P:cell adhesion; IEA.
InterPro; IRR000742; EGF 2.
InterPro; IRR000742; EGF 2.
InterPro; IRR005099; EGF 2.
InterPro; IRR00509; EGF 2.
InterPro; IRR00509; EGF 2.
InterPro; IRR0060109; EGF 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-like domain, Glycoprotein.
SEQUENCE 5374 AA, 579545 MW, 90D2D8CFESDE24EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 EGF-like domain.
                                                                         Last sequence update)
Last annotation update)
                                PRT; 5374 AA.
                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00022; EGF 1; UNKNOWN 1.
PROSITE; PS01186; EGF 2; 18.
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VWF C.
VWF D.
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF312033; AAK28824.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; PF00629; MAM; 3.
; PF01826; TIL; 25.
; PF02345; TIL_assoc; 25.
; PF001094; VWD; 4.
T; SM00181; EGF; 2.
T; SM00274; FOLN; 20.
T; SM00214; VWC; 18.
T; SM00216; VWD; 4.
                                                                         01-JUN-2001 (TrEMBLrel. 17, 05-JUL-2004 (TrEMBLrel. 27,
                                                           17,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR006210; IEGF.
InterPro; IPR000998; MAM.
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hes 14; Conservative
                              PRELIMINARY;
                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50026; EGF PS50060; MAM 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:106656; Zan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterPro; IPR003328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001007;
InterPro; IPR001846;
                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q90248; 1HX2
                                                                                                     ZAN (Zonadhesin).
                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                          STRAIN=129/Sv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00008;
                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/Sv;
                                                           01-JUN-2001
                                                                                                                    Name=Zan:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                             00N660
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SMART;
SMART;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART
RESULT 12
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RA Gao Z., Harumi T., Garbers D.L.;

R. "Chromosome localization of the mouse zonadhesin gene and the human chromosome localization of the mouse zonadhesin gene (ZAN).";

Zonadhesin gene (ZAN).";

Genomics 41:119-122(1997).

- FUNCTION: Binds in a species-specific manner to the zona pellucida of the egg. May be involved in gamete recognition and/or signaling.

- SUBBUIT: Probably forms covalent oligomers.

- SUBBUIT: Probably forms covalent oligomers.

- SUBBUIT: Probably forms covalent oligomers.

- SUBCILLUAR LOCATION: Type I membrane protein, exclusively on the apical region of the sperm head.

- ITISSUB SPECIFICITY: In testis, primarily in haploid spermatids.

- IDOMAIN: The MAM domains probably mediates sperm adhesion to the zona pellucida.

- IDOMAIN: During sperm migration through the reproductive tracts, the mucin-like domain might inhibit inappropriate trapping of spermatozoa or promoting adhesion to the oviductal isthmus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstarion the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                 Gao Z., Garbers D.L.;
"Species diversity in the structure of zonadhesin, a sperm-specific
membrane protein containing multiple cell adhesion molecule-like
                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 4864-5376 FROM N.A.
TISSUE=Testis;
MEDLINE=97271566; PubMed=9126492; DOI=10.1006/geno.1997.4620;
                                                                                                                                                                                                                                              TISSUE=Testis;
MEDLINE=98123114; PubMed=9452463; DOI=10.1074/jbc.273.6.3415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).
--- SIMILARITY: Contains 1 EGF-like domain.
--- SIMILARITY: Contains 3 MAM domains.
--- SIMILARITY: Contains 25 VWFD domains.
                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 273:3415-3421(1998).
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InterPro; IPR000742; BGF 2.
InterPro; IPR006209; BGF_like.
InterPro; IPR000998; MAM.
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fam; PF00094; VWD; 4.
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PROSITE; PS01186; EGF 2; 18.
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fam; PF00629; MAM; 3.
fam; PF01826; TIL; 25.
                                                                                                                              Mus musculus (Mouse).
                                                                                             Zonadhesin precursor.
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                                                                                                                 Name=Zan;
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5; Mismatches 16; Indels

3297 QCPTNSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC 3334

7 OCSONEYFDSLLHACIP-COLRCSSNTP--PLTCQRYC 41

3

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01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2001 (TrEMBLrel. 26, Last annotation update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
07-NAR-2004 (TrEMBLrel. 26, Last annotation update)
08-NARMES=T10E10.4, T10E10.4;
Caenorhabditis elegans.
Elwaryota; Metazca; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                    Gaps
 4586 4586 N-linked (GlCNAC. .) (Potential).
5136 N-linked (GLCNAC. .) (Potential).
5252 5525 N-linked (GLCNAC. .) (Potential).
5376 AA; 579908 MW; 0E44DB77DF2A2620 CRC64;
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STRANTE-BLISETON N2;
MEDILINE-99069613; PubMed-9851916;
WormBase Consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
science 282:2012-2018(1998).
                                                         Query Match 24.6%; Score 69.5; DB 1; Length 5376; Best Local Similarity 36.8%; Pred. No. 36; Matches 14; Conservative 5; Mismatches 16; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; U35644; AAA80360.2; -.
EMBL; U35644; AAA80360.2; -.
EMBL; U35644; AAA80360.2; -.
EMSP; P10969; 1WGT.
R WormBase; WBGene00020421; T10E10.4.
R WormBase; WBGene00020421; T10E10.4.
R WormPep; T10E10.4; CE25989.
R GO; GO:0005576; C:extracellular; IEA.
R GO; GO:0005576; C:extracellular; IEA.
R GO; GO:0005576; C:extracellular; IEA.
R GO; GO:0005576; C:extracellular; IEA.
R GO; GO:0005576; C:extracellular; IEA.
R InterPro; IPR00527; C:extracellular; IEA.
R InterPro; IPR00527; Chitin_bind_PerA.
R InterPro; IPR00517; Chitin_bind_PerA.
R InterPro; IPR00517; Chitin_bind_PerA.
R InterPro; IPR00517; Chitin_bind_PerA.
R InterPro; IPR00517; Chitin_bind_PerA.
R InterPro; IPR00517; Chitin_bind_PerA.
R InterPro; IPR00517; Chitin_bind_PerA.
R InterPro; IPR00517; Chitin_bind_PerA.
R InterPro; IPR00517; Chitin_bind_PerA.
R InterPro; IPR00517; Chitin_bind_PerA.
R INTERPRO; IPR006150; Worm_repeat_1.
R SMART; SM00181; EGF.
R SMART; SM00289; WRR1; 12.
R PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The sequence of C. elegans cosmid T10E10."; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston R.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
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                                                                                                                      3299 QCPTNSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC 3336
                                                                                                         7 QCSQNEYFDSLLHACIP-CQLRCSSNTP--PLTCQRYC 41
                                                                                                                                                                                         PRELIMINARY;
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STRAIN-Bristol N2;
Geisel C.;
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80 X heptapeptide repeats (approximate)
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PROSITE; PS50026; EGF_3; 1.
PROSITE; PS00740; MAM_1; FALSE_NEG.
PROSITE; PS50060; MAM_2; 3.
PROSITE; PS50060; MAM_2; 3.
Cell adhesion; EGF_like domain; Glycoprotein; Repeat; Signal; Transmembrane.
                                                                      Zonadhesin.
Extracellular (Potential).
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WWFD 9 (partial).
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WWFD 11 (partial).
WWFD 12 (partial).
WWFD 13 (partial).
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WWFD 14 (partial).
WWFD 15 (partial).
WWFD 16 (partial).
WWFD 17 (partial).
WWFD 19 (partial).
WWFD 20 (partial).
WWFD 21 (partial).
WWFD 22 (partial).
WWFD 23 (partial).
WWFD 24 (partial).
WWFD 25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NOSI_TaxID=9606;
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                                                                                                   Query Match 24.2%; Score 68.5; DB 2; Length 966; Best Local Similarity 36.2%; Pred. No. 8.2; Matches 17; Conservative 10; Mismatches 15; Indels E
                                                                                                                                                                                                                                   215 QCSQSTVFNSDLNVCVPLAIQNSCDSSTQQPVCS--C-SQVSSSCPG 258
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InterPro; IPR002919; Cysrich Til.

InterPro; IPR009041; PMP_SGGT.

InterPro; IPR001846; VWF_D.

Fean, PR01826; TIL; 2.

Fean, PR001845; VWC_out; 2.

SMART; SM00215; VWC_out; 2.

SMART; SM00216; VWC_ out; 2.

SMART; SM00216; VWC_ out; 3.

NOW TER 1569 AA; 168065 WW; 6AEDEE143ECB855B CRC64;
                                                                                                                                                                                                      7 QCSQNEYFDSLLHACIPCQLR--CSSNTPPLTCQRYCNASVTNSVKG 51
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PubMed=15081123; DOI=10.1016/j.ygeno.2003.11.003;
Rousseau K., Byrne C., Kim Y.S., Gum J.R., Swallow D.M., Toribara N.W.;
PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 966 AA; 102460 MW; B565A3CDD25216D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Mucin glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1569 AA
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Search completed: February 26, 2005, 21:00:50 Job time : 51.0468 secs

1179 CSQDEYFDHEEGVCVPCM-----PPTTPQ 1202

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